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O I 0 IntelliGenetics  
> 0 <

FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file us-09-820-790b-3.res made by tport on Fri 10 Oct 103 17:36:22-PDT.

Query sequence being compared: US-09-820-790B-3 (1-28438)  
Number of sequences searched: 1  
Number of scores above cutoff: 1

Results of the initial comparison of US-09-820-790B-3 (1-28438) with:  
File: ac006454.seq

100-  
N  
U  
M  
B  
E  
R  
O  
F  
S  
E  
Q  
U  
E  
N  
C  
E  
S  
0  
SCORE 0 1435 2870 4305 5740 7174 8609 10044 11479 12914  
SIDEV  
\*  
*\* Please note: This alignment program  
can only handle segs with a max length  
of 25,000. So it truncated seg ID 3  
to 25,000.*

## PARAMETERS

Similarity matrix Unitary  
Mismatch penalty 1  
Gap penalty 5.00  
Gap size penalty 0.33  
Cutoff score 1  
Randomization group 0

## SEARCH STATISTICS

Scores: Mean 12914 Median 0 Standard Deviation 0.00  
Times: CPU 00:00:37.03 Total Elapsed 00:00:38.00

Number of residues: 153203  
Number of sequences searched: 1  
Number of scores above cutoff: 1

The scores below are sorted by initial score.  
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name Description Length Score Init. Opt.  
1. ac006454 TOIG of: ac006454 check: 891 153203 12914 24880 0.00 0

1. US-09-820-790B-3 (1-28438)  
ac006454 TOIG of: ac006454 check: 8918 from: 1 to: 15320

Initial Score = 12914 Optimized Score = 24880 Significance = 0.00  
Residue Identity = 99% Matches = 24980 Mismatches = 7  
Gaps = 20 Conservative Substitutions = 0

X 10 20 30 40 50 60 70  
GAGCTGCTGCTCTCTCTCCAGGAGGAGGCTGTGGGTTGAGGCTCAGCGTCTGGGACTCTGGGG  
GAGCTGCTGCTCTCTCTCCAGGAGGAGGCTGTGGGTTGAGGCTCAGCGTCTGGGACTCTGGGG  
8840 8850 8860 8870 8880 8890 8900  
80 90 100 110 120 130 140  
TGAAGGCTCAGCCATGCTCTCCAGGAGGAGGCTGTGGGTTGAGGCTCAGCGTCTGGGACTCTGGGG  
TGAAGGCTCAGCCATGCTCTCCAGGAGGAGGCTGTGGGTTGAGGCTCAGCGTCTGGGACTCTGGGG  
8910 8920 8930 8940 8950 8960 8970  
150 160 170 180 190 200 210  
CTGTTTCTCTGTTTGTAAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCA  
CTGTTTCTCTGTTTGTAAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCAACCCCA  
8980 8990 9000 9010 9020 9030 9040 9050  
220 230 240 250 260 270 280  
GTGCGGTCACCTCTGAGCGGAGAACTGTTCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
GTGCGGTCACCTCTGAGCGGAGAACTGTTCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
9060 9070 9080 9090 9100 9110 9120  
290 300 310 320 330 340 350 360  
GAGACTTCGCGCTAGCTATCGAGGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
GAGACTTCGCGCTAGCTATCGAGGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
9130 9140 9150 9160 9170 9180 9190 9200  
370 380 390 400 410 420 430  
GTGTTGCTGCGCTAGCTATCGAGGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
GTGTTGCTGCGCTAGCTATCGAGGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
9200 9210 9220 9230 9240 9250 9260 9270  
440 450 460 470 480 490 500  
TTTCGCTGCGCACACGAGGCTACCTGTCCTGAGGTCCTTCGCAAGAGGAGGAGGAGGAGGAGGAGG  
TTTCGCTGCGCACACGAGGCTACCTGTCCTGAGGTCCTTCGCAAGAGGAGGAGGAGGAGGAGGAGG  
9270 9280 9290 9300 9310 9320 9330 9340  
510 520 530 540 550 560 570  
CTGGGCTGCTGAGGCTGCGCTGAGTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
CTGGGCTGCTGAGGCTGCGCTGAGTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
9340 9350 9360 9370 9380 9390 9400 9410  
580 590 600 610 620 630 640  
CATCTGGAGTGTGAGTGTGAGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG  
CATCTGGAGTGTGAGTGTGAGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG  
9420 9430 9440 9450 9460 9470 9480 9490  
650 660 670 680 690 700 710 720  
CTGCCCTGGAGGCTGCTGCCACAGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
CTGCCCTGGAGGCTGCTGCCACAGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
9490 9500 9510 9520 9530 9540 9550 9560















11230 11240 11250 11260 11270 11280 11290 11300  
TAGGCTTCCTGAGGCTGAGAGGCGCTGATCTCAGAGCTGATCTTGGCCCTCTCTGCTGCTCTCC  
TAGGCTTCCTGAGGCTGAGAGGCGCTGATCTCAGAGCTGATCTTGGCCCTCTCTGCTGCTCTCC  
20070 20080 20090 20100 20110 20120 20130  
11310 11320 11330 11340 11350 11360 11370  
ACCCACCTCCTCAGTGGGCGCCGAGCTGCTCTGAGAGAGCCCTCCCTCTCTGCTTCCCTCTCTG  
ACCCACCTCCTCAGTGGGCGCCGAGCTGCTCTGAGAGAGCCCTCCCTCTCTGCTTCCCTCTCTG  
20140 20150 20160 20170 20180 20190 20200  
11380 11390 11400 11410 11420 11430 11440  
TCTGGCATCAGTCCCATCAGTGGGCTGATCTCAGAGCTGAGAGGCGCTCTCTGCTGCTGCTG  
TCTGGCATCAGTCCCATCAGTGGGCTGATCTCAGAGCTGAGAGGCGCTCTCTGCTGCTGCTG  
20210 20220 20230 20240 20250 20260 20270  
11450 11460 11470 11480 11490 11500 11510  
TGGAGGATGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
TGGAGGATGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
20280 20290 20300 20310 20320 20340 20350  
11520 11530 11540 11550 11560 11570 11580  
CTCCAGGCTCCTCAGTGGGCTGCTTACAGAGGCGCCGAGGCTCTCTGCTGCTGCTGCTGCTG  
CTCCAGGCTCCTCAGTGGGCTGCTTACAGAGGCGCCGAGGCTCTCTGCTGCTGCTGCTGCTG  
20360 20370 20380 20390 20400 20410 20420  
11590 11600 11610 11620 11630 11640 11650  
TTCCTCTGCGGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
TTCCTCTGCGGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
20430 20440 20450 20460 20470 20480 20490  
11670 11680 11690 11700 11710 11720 11730  
CAGAG  
CAGAG  
20500 20510 20520 20530 20540 20550 20560  
11740 11750 11760 11770 11780 11790 11800  
CCTGGAG  
CCTGGAG  
20570 20580 20590 20600 20610 20620 20630  
11810 11820 11830 11840 11850 11860 11870  
GAGCTGAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG  
GAGCTGAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG  
20640 20650 20660 20670 20680 20690 20700  
11880 11890 11900 11910 11920 11930 11940  
AGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
AGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
20710 20720 20730 20740 20750 20760 20770  
11950 11960 11970 11980 11990 12000 12010  
CTGGGAG  
CTGGGAG  
20790 20800 20810 20820 20830 20840 20850  
12030 12040 12050 12060 12070 12080 12090  
AAGGAG  
AAGGAG  
20860 20870 20880 20890 20900 20910 20920  
12100 12110 12120 12130 12140 12150 12160

TGTGGGAGAGAGTGTCTGCTGGGCGAGGCGAGGCTTCTTGAGAGCCCTGTGCGATCTGAGAGCTC  
TGTGGGAGAGAGTGTCTGCTGGGCGAGGCGAGGCTTCTTGAGAGCCCTGTGCGATCTGAGAGCTC  
20930 20940 20950 20960 20970 20980 20990  
12170 12180 12190 12200 12210 12220 12230  
CTGGAGAGGCTGCTGCTGATTTGGATGAGAGCGGCTGCTTCAATTTGAGAGGAGGAGGAGGAGGAG  
CTGGAGAGGCTGCTGCTGATTTGGATGAGAGCGGCTGCTTCAATTTGAGAGGAGGAGGAGGAGGAG  
21000 21010 21020 21030 21040 21050 21060  
CTGGAGAGGCTGCTGATTTGGATGAGAGCGGCTGCTTCAATTTGAGAGGAGGAGGAGGAGGAGGAG  
21070 21080 21090 21100 21110 21120 21130  
TGTACGCTGGAATTTGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
TGTACGCTGGAATTTGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
21140 21150 21160 21170 21180 21190 21200  
CTGGAGAGGCTGCTGCTGATTTGGATGAGAGCGGCTGCTTCAATTTGAGAGGAGGAGGAGGAGGAG  
CTGGAGAGGCTGCTGCTGATTTGGATGAGAGCGGCTGCTTCAATTTGAGAGGAGGAGGAGGAGGAG  
21210 21220 21230 21240 21250 21260 21270  
12310 12320 12330 12340 12350 12360 12370  
CTGGAGAGGCTGCTGCTGATTTGGATGAGAGCGGCTGCTTCAATTTGAGAGGAGGAGGAGGAGGAG  
CTGGAGAGGCTGCTGCTGATTTGGATGAGAGCGGCTGCTTCAATTTGAGAGGAGGAGGAGGAGGAG  
21280 21290 21300 21310 21320 21330 21340  
12390 12400 12410 12420 12430 12440 12450  
GTGGAGGCGGCTGCTGCTGATTTGGATGAGAGCGGCTGCTTCAATTTGAGAGGAGGAGGAGGAGGAG  
GTGGAGGCGGCTGCTGCTGATTTGGATGAGAGCGGCTGCTTCAATTTGAGAGGAGGAGGAGGAGGAG  
21260 21270 21280 21290 21300 21310 21320  
12460 12470 12480 12490 12500 12510 12520  
CCCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
CCCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
21290 21300 21310 21320 21330 21340 21350  
12530 12540 12550 12560 12570 12580 12590  
CCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
CCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
21360 21370 21380 21390 21400 21410 21420  
12600 12610 12620 12630 12640 12650 12660  
TCAGTTGAGAGGCTGCTGCTGATTTGGATGAGAGCGGCTGCTTCAATTTGAGAGGAGGAGGAGGAG  
TCAGTTGAGAGGCTGCTGCTGATTTGGATGAGAGCGGCTGCTTCAATTTGAGAGGAGGAGGAGGAG  
21430 21440 21450 21460 21470 21480 21490  
12670 12680 12690 12700 12710 12720 12730  
ATCCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
ATCCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
21500 21510 21520 21530 21540 21550 21560  
12750 12760 12770 12780 12790 12800 12810  
TAGAGGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
TAGAGGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
21580 21590 21600 21610 21620 21630 21640  
12820 12830 12840 12850 12860 12870 12880  
GCTCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
GCTCTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
21650 21660 21670 21680 21690 21700 21710  
12890 12900 12910 12920 12930 12940 12950  
GCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
GCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG  
21720 21730 21740 21750 21760 21770 21780  
12960 12970 12980 12990 13000 13010 13020  
CAGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG







[illegible]





20880	20890	20900	20910	20920	20930	20940
ACACATGATGAGCACACCCGGGCATGGCGCTCTTTGTGACTCAGTCCACTGCGCAGGTGGGCTCC						
ACACATGATGAGCACACCCGGGCATGGCGCTCTTTGTGACTCAGTCCACTGCGCAGGTGGGCTCC						
29710	29720	29730	29740	29750	29760	29770
20950	20960	20970	20980	20990	21000	21010
TGTGGTGTGAGCTCCACGAGGTGGCGAGAGAAAGCAACCCACACAGCGCTGCTGAGAATTC						
TGTGGTGTGAGCTCCACGAGGTGGCGAGAGAAAGCAACCCACACAGCGCTGCTGAGAATTC						
29780	29790	29800	29810	29820	29830	29840
21020	21030	21040	21050	21060	21070	21080
CCCTCTTGCTGGGCAAGTGGCTCATACCTTAATCCAGCACTTTGGGAGCCGAGTGGGCAATCAC						
CCCTCTTGCTGGGCAAGTGGCTCATACCTTAATCCAGCACTTTGGGAGCCGAGTGGGCAATCAC						
29850	29860	29870	29880	29890	29900	29920
TTGAGTTAGAGGTTTGACACCGCTGGCGCAATAGTGAACCTCATCTCCACTAAAATAATACACAC						
29930	29940	29950	29960	29970	29980	29990
21100	21110	21120	21130	21140	21150	21160
TTGAGTTAGAGGTTTGACACCGCTGGCGCAATAGTGAACCTCATCTCCACTAAAATAATACACAC						
29990	30000	30010	30020	30030	30050	30060
AAAATATAGCTGGGTGGTGGTGACCTGTAGTTCACGCTACTCGGAGGCTGAGGACAGAGAAATCGCT						
AAAATATAGCTGGGTGGTGGTGACCTGTAGTTCACGCTACTCGGAGGCTGAGGACAGAGAAATCGCT						
30070	30080	30090	30100	30110	30120	30130
21240	21250	21260	21270	21280	21290	21300
TGAACCTGGAGTCCAGAGCTCAGTGTAGCGGAGATCATGTCACTGCACGCCGGGTGACAGAGTGAG						
TGAACCTGGAGTCCAGAGCTCAGTGTAGCGGAGATCATGTCACTGCACGCCGGGTGACAGAGTGAG						
30070	30080	30090	30100	30110	30120	30130
21310	21320	21330	21340	21350	21360	21370
ACTCCATCTFAAAAAAAGAAATCCCTCTCTGGGAATTTAGACACAGAGGTTCATGTATGTGGC						
ACTCCATCTFAAAAAAAGAAATCCCTCTCTGGGAATTTAGACACAGAGGTTCATGTATGTGGC						
30140	30150	30160	30170	30180	30190	30200
21380	21390	21400	21410	21420	21430	21440
CGTTGGAGCAGCACTCACAGCAAAAGTGGAAACCTCACACAGGCGCTCTTGGTGAATAATGTGTC						
CGTTGGAGCAGCACTCACAGCAAAAGTGGAAACCTCACACAGGCGCTCTTGGTGAATAATGTGTC						
30210	30220	30230	30240	30250	30260	30270
21460	21470	21480	21490	21500	21510	21520
CTGACGGCGGCGACGTGTTTGAGGCGAGGTTCACAGTGGCGCTTGACAGAGCTGCTGCTTCGGTGCACCTTCGGGG						
CTGACGGCGGCGACGTGTTTGAGGCGAGGTTCACAGTGGCGCTTGACAGAGCTGCTGCTTCGGGG						
30290	30300	30310	30320	30330	30340	30350
21530	21540	21550	21560	21570	21580	21590
CAGTGTGGGAGTGCAGAGCTTCCCCACAGAGGAGGTTCCAGAGAACCTGCTTCCGGTGCACCTTCGGGG						
CAGTGTGGGAGTGCAGAGCTTCCCCACAGAGGAGGTTCCAGAGAACCTGCTTCCGGTGCACCTTCGGGG						
30360	30370	30380	30390	30400	30410	30420
21600	21610	21620	21630	21640	21650	21660
GTTTGGAGTTTTTCCACGACGAATTAATTGAGAAACCACTGTTACTCGTGTGTATAGTGAAGGTCGCTG						
GTTTGGAGTTTTTCCACGACGAATTAATTGAGAAACCACTGTTACTCGTGTGTATAGTGAAGGTCGCTG						
30430	30440	30450	30460	30470	30480	30490
21670	21680	21690	21700	21710	21720	21730
TGCATGTGTTCTGTGTGAGTGTGCAATGATGTGGTGCCCTGGGTATATATCTTCGCAGATACGCTGAG						
TGCATGTGTTCTGTGTGAGTGTGCAATGATGTGGTGCCCTGGGTATATATCTTCGCAGATACGCTGAG						
30500	30510	30520	30530	30540	30550	30560



TGTTCACAGTCTGTGGCCACAGACAGCCAGCCGATCCACAGACCCATCTCTGAAACCCACAGCTGCACGCATCTT  
 32300 32310 32320 32330 32340 32350 32360 32370 32380 32390 32400 32410 32420 32430 32440  
 32450 32460 32470 32480 32490 32500 32510 32520 32530 32540 32550 32560 32570 32580 32590  
 32600 32610 32620 32630 32640 32650 32660 32670 32680 32690 32700 32710 32720 32730 32740  
 32750 32760 32770 32780 32790 32800 32810 32820 32830 32840 32850 32860 32870 32880  
 32890 32900 32910 32920 32930 32940 32950 32960 32970 32980 32990 33000 33010 33020  
 33030 33040 33050 33060 33070 33080 33090 33100 33110 33120 33130 33140 33150 33160  
 33170 33180 33190 33200 33210 33220 33230 33240 33250 33260 33270 33280 33290 33300  
 33310 33320 33330 33340 33350 33360 33370 33380 33390 33400 33410 33420 33430 33440  
 33450 33460 33470 33480 33490 33500 33510 33520 33530 33540 33550 33560 33570 33580  
 33590 33600 33610 33620 33630 33640 33650 33660 33670 33680 33690 33700 33710 33720  
 33730 33740 33750 33760 33770 33780 33790 33800 33810 33820 33830 33840 33850 33860  
 33870 33880 33890 33900 33910 33920 33930 33940 33950 33960 33970 33980 33990 34000  
 34010 34020 34030 34040 34050 34060 34070 34080 34090 34100 34110 34120 34130 34140 34150  
 34160 34170 34180 34190 34200 34210 34220 34230 34240 34250 34260 34270 34280 34290  
 34300 34310 34320 34330 34340 34350 34360 34370 34380 34390 34400 34410 34420 34430  
 34440 34450 34460 34470 34480 34490 34500 34510 34520 34530 34540 34550 34560 34570 34580  
 34590 34600 34610 34620 34630 34640 34650 34660 34670 34680 34690 34700 34710 34720  
 34730 34740 34750 34760 34770 34780 34790 34800 34810 34820 34830 34840 34850 34860  
 34870 34880 34890 34900 34910 34920 34930 34940 34950 34960 34970 34980 34990 35000  
 35010 35020 35030 35040 35050 35060 35070 35080 35090 35100 35110 35120 35130 35140  
 35150 35160 35170 35180 35190 35200 35210 35220 35230 35240 35250 35260 35270 35280  
 35290 35300 35310 35320 35330 35340 35350 35360 35370 35380 35390 35400 35410 35420  
 35430 35440 35450 35460 35470 35480 35490 35500 35510 35520 35530 35540 35550 35560  
 35570 35580 35590 35600 35610 35620 35630 35640 35650 35660 35670 35680 35690 35700  
 35710 35720 35730 35740 35750 35760 35770 35780 35790 35800 35810 35820 35830 35840  
 35850 35860 35870 35880 35890 35900 35910 35920 35930 35940 35950 35960 35970 35980  
 35990 36000 36010 36020 36030 36040 36050 36060 36070 36080 36090 36100 36110 36120  
 36130 36140 36150 36160 36170 36180 36190 36200 36210 36220 36230 36240 36250 36260  
 36270 36280 36290 36300 36310 36320 36330 36340 36350 36360 36370 36380 36390 36400  
 36410 36420 36430 36440 36450 36460 36470 36480 36490 36500 36510 36520 36530 36540  
 36550 36560 36570 36580 36590 36600 36610 36620 36630 36640 36650 36660 36670 36680  
 36690 36700 36710 36720 36730 36740 36750 36760 36770 36780 36790 36800 36810 36820  
 36830 36840 36850 36860 36870 36880 36890 36900 36910 36920 36930 36940 36950 36960  
 36970 36980 36990 37000 37010 37020 37030 37040 37050 37060 37070 37080 37090 37100  
 37110 37120 37130 37140 37150 37160 37170 37180 37190 37200 37210 37220 37230 37240  
 37250 37260 37270 37280 37290 37300 37310 37320 37330 37340 37350 37360 37370 37380  
 37390 37400 37410 37420 37430 37440 37450 37460 37470 37480 37490 37500 37510 37520  
 37530 37540 37550 37560 37570 37580 37590 37600 37610 37620 37630 37640 37650 37660  
 37670 37680 37690 37700 37710 37720 37730 37740 37750 37760 37770 37780 37790 37800  
 37810 37820 37830 37840 37850 37860 37870 37880 37890 37900 37910 37920 37930 37940  
 37950 37960 37970 37980 37990 38000 38010 38020 38030 38040 38050 38060 38070 38080  
 38090 38100 38110 38120 38130 38140 38150 38160 38170 38180 38190 38200 38210 38220  
 38230 38240 38250 38260 38270 38280 38290 38300 38310 38320 38330 38340 38350 38360  
 38370 38380 38390 38400 38410 38420 38430 38440 38450 38460 38470 38480 38490 38500  
 38510 38520 38530 38540 38550 38560 38570 38580 38590 38600 38610 38620 38630 38640  
 38650 38660 38670 38680 38690

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: October 10, 2003, 08:10:41 ; Search time 5750 Seconds  
(without alignments)  
3671.194 Million cell updates/sec

Title: US-09-820-790B-2

Perfect score: 2715  
Sequence: 1 MATVTCTRTFDYQLYEDI.....DGKQWVHFHCGAPVAPLQ 516

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame\_p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO\_spool/US09820790/runat\_09102003\_170018\_14763/app\_query.fasta\_1.711  
-DB=GenEmbl -QFAST=FASTAP -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09820790.scgn 1.1 3635 @runat\_09102003\_170018\_14763 -NCPU=6 -ICPU=3  
-NO\_MMAPP -LARGEQUERY -NGG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*

1: gb.ba.\*

2: gb.rtg.\*

3: gb.in.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pl.\*

9: gb.pr.\*

10: gb.ro.\*

11: gb.sts.\*

12: gb.sy.\*

13: gb.un.\*

14: gb.vi.\*

15: em.ba.\*

16: em.fun.\*

17: em.hum.\*

18: em.in.\*

19: em.mu.\*

20: em.cm.\*

21: em.or.\*

22: em.ov.\*

23: em.pat.\*

24: em.ph.\*

25: em.pl.\*

26: em.ro.\*

27: em.sts.\*

28: em.un.\*

29: em.vi.\*  
30: em.htg.hum.\*  
31: em.htg.inv.\*  
32: em.htg.other.\*  
33: em.htg.mus.\*  
34: em.htg.pln.\*  
35: em.htg.rod.\*  
36: em.htg.mam.\*  
37: em.htg.vrt.\*  
38: em.sy.\*  
39: em.htgo.hum.\*  
40: em.htgo.mus.\*  
41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query			DB ID	Description
		Match	Length	%		
1	2692	99.2	1727	9	AF078803	AF078803 Homo sapi
2	2683	98.8	1825	9	AF112472	AF112472 Homo sapi
3	2672	98.4	3830	10	MNCAMK2	X63615 M.musculus
4	2669	98.3	1840	10	RATPKCA	M16112 Rat brain t
5	2621	96.5	2220	9	HSU23460	U23460 Human proli
6	2572	94.7	1577	9	AF081924	AF081924 Homo sapi
7	2571	94.7	1703	5	AF085249	AF085249 Gallus ga
8	2549	93.9	1557	9	HSU252238	AJ252238 Homo sapi
9	2548.5	93.9	1653	9	AF083419	AF083419 Homo sapi
10	2539.5	93.5	1750	9	AF112471	AF112471 Homo sapi
11	2526	93.0	2508	5	XLJ06636	U06636 Xenopus lae
12	2484.5	90.4	1610	9	AF081572	AF081572 Homo sapi
13	2450.5	90.3	1764	9	HSU252236	AJ252236 Homo sapi
14	2450.5	90.3	1905	9	BC019070	BC019070 Homo sapi
15	2431.5	89.9	2564	5	XLJ18196	U18196 Xenopus lae
16	2374.5	87.5	1979	10	RNCCDPPK2	X83375 R.norvegicu
17	2317.5	85.4	1775	9	HSU252237	AJ252237 Homo sapi
18	2286.5	84.2	1930	4	AF464186	AF464186 Mustela p
19	2286.5	84.2	1941	4	SSU72973	U72973 Sus scrofa
20	2256	83.1	2080	5	AF233631	AF233631 Xenopus l
21	2250.5	82.9	1728	10	RATPK2G	J04063 Rat calmodu
22	2248.5	82.8	3736	9	BC034044	BC034044 Homo sapi
23	2241	82.6	1829	4	AF464185	AF464185 Mustela p
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25	2230	82.1	1793	9	HUMCCDPKB	L07044 Homo sapien
26	2230	82.1	1838	4	AF464184	AF464184 Mustela p
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28	2230	82.1	1864	10	BC019162	BC019162 Mus muscu
29	2225.5	82.0	2384	5	AF233633	AF233633 Xenopus l
30	2224.5	81.9	1926	5	BC049002	BC049002 Xenopus l
31	2223	81.9	1829	4	D14905	D14905 Oryctolagus
32	2216	81.6	1764	10	S71570	S71570 Ca2+/calmod
33	2215.5	81.6	1823	10	AF395884	AF395884 Mus muscu
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35	2186.5	80.5	1757	4	SSU72971	U72971 Sus scrofa
36	2186.5	80.5	1775	4	AF464182	AF464182 Mustela p
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41	2172.5	80.0	1448	9	AF140350	AF140350 Homo sapi
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227

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Db 1444 CCACAGTGCAGCTCAFTTGGAGAGATGCGCGCTGATCGCTTACATCCGGCTCAGCGAG 1503

QY 475 TyrIleAspGlyGlnGlyArgProArgThrSerGlnSerGluGluThrArgValTrpHis 494

Db 1504 TACATTACGCGGAGGCGCGCGCCAGCACAGGAGCTCTGAGGAGACCGCGTGTGGCAC 1563

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QY 515 LeuGln 516

Db 1624 CTGCAG 1629

RESULT 2

AF112472 1825 bp mRNA linear PRI 10-JAN-1999

LOCUS Homo sapiens calcium/calmodulin-dependent protein kinase II beta

DEFINITION subunit mRNA, complete cds.

ACCESSION AF112472

VERSION AF112472.1 GI:4139269

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1825)

AUTHORS Li, G.Y. and Cooper, N.G.F.

TITLE Molecular cloning and sequencing of human calcium/calmodulin dependent protein kinase II beta subunit

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1825)

AUTHORS Li, G.Y. and Cooper, N.G.F.

TITLE Direct Submission

JOURNAL Submitted (09-DEC-1998) Anatomical Sciences & Neurobiology, University of Louisville, 500 Preston Street, Louisville, KY 40292, USA

FEATURES

source Location/Qualifiers

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BASE COUNT 420 a 567 c 510 g 327 t 1 others

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Pred. No.: 1,61e-191 Length: 1825

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Best Local Similarity: 94.83% Mismatches: 1

Query Match: 26

DB: 9 Gaps: 1

US-09-820-790B-2 (1-516) x AF112472 (1-1825)

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Db 167 GCAGCCACAGATCATCACACCAAGAGCTGTACGACAGATCACCAAGAGCTGGAGAGA 226

QY 61 GluAlaArgIleCysArgLeuLeuLysHisSerAsnIleValArgLeuHisAspSerIle 80

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QY 81 SerGluGluGlyPheHisTyrLeuValPheAspLeuValThrGlyGlyGluLeuPheGlu 100

Db 287 TCCGAGGAGGGCTTCCACTAGCTCTTTCGATCTGTGCTGCTGCTGCTGCTGCTGCTGCT 346

QY 101 AspIleValAlaArgGluYrTyrSerGluAlaAspAlaSerHisCysIleGlnGlnIle 120

Db 347 GACATGTGGCAGAGAGTACTACAGCGAGCTGTGAGTGCAGTCTACTATCAGCAGATC 406

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QY 221 LysLeuYrGlnGlnIleLysAlaGlyAlaYrAspPheProSerProGluTrpAspThr 240

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Db      1007  ACGCTCGGCGCACAAATGTCACCGCGGCTCCGCGCACCATCCAGGCTGGTGGAAACA 1066
QY      341  AlaLysSerLeuLeuAsnLysLysAlaAspGlyValLysProGlnThrAsnSerThrLys 360
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QY      361  AsnSerAlaAlaAlaThrSerProLysGlyThrLeuProProAlaAlaLeuGluProGln 380
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Db      1667  CTGCAG 1672

RESULT 3
LOCUS   MMCAMK2
DEFINITION M.musculus Camk-2 mRNA for Ca2+/calmodulin dependent protein kinase
          II beta subunit.
ACCESSION X63615.1
VERSION   X63615.1 GI:50275
KEYWORDS  calcium/calmodulin-dependent protein; calmodulin; Camk-2 gene;
          protein kinase; Ser and Thr phosphorylating.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
          1 (bases 1 to 3830)
          Direct Submission
          Harbers K.
          Submitted (23-DEC-1991) K. Harbers, Heinrich Pette Institut,
          Martinistr. 52, 2000 Hamburg 20, FRG
REFERENCE 2 (bases 1 to 3830)
AUTHORS   Karls, J., Muller, J., Gilbert, D.J., Copeland, N.G., Jenkins, N.A. and
          Harbers, K.
          Structure, expression, and chromosome location of the gene for the

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beta subunit of brain-specific Ca2+/calmodulin-dependent protein
kinase II identified by transgene integration in an embryonic
lethal mouse mutant
Mol. Cell. Biol. 12 (8), 3644-3652 (1992)
92334366
PUBMED 1321343
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 DEFINITION Rat brain type II Ca2+/calmodulin-dependent protein kinase beta subunit mRNA, complete cds.  
 ACCESSION M16112.1 GI:206170  
 VERSION calcium/calmodulin-dependent protein kinase; protein kinase.  
 KEYWORDS Rattus norvegicus (Norway rat)  
 SOURCE Rattus norvegicus  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.  
 REFERENCE 1 (bases 1 to 1840)  
 AUTHORS Bennett,M.K. and Kennedy,M.B.  
 TITLE Deduced primary structure of the beta subunit of brain type II Ca2+/calmodulin-dependent protein kinase determined by molecular cloning  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 84 (7), 1794-1798 (1987)  
 MEDLINE 87175563  
 PUBMED 3470758  
 COMMENT Original source text: Rat (Sprague Dawley) brain, cDNA to mRNA, clone lambda-10-beta-5-2.  
 Draft entry and computer-readable sequence for [1] kindly provided by M.B.Kennedy, 18-MAY-1987.  
 Nucleotides 1194-1238 were missing from two clones, without shifting the reading frame. There may be an alternatively spliced beta subunit message.  
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Best Local Similarity: 94.28%  
 Query Match: 98.31%  
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 Indels: 26  
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US-09-820-790b-2 (1-516) x RANPKCA (1-1840)

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 REFERENCE 1 (bases 1 to 2220)  
 AUTHORS Leddy,J.J., Saih,M. and Tuana,B.S.  
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 JOURNAL Submitted (24-MAR-1995) John J. Leddy, Pharmacology, University of  
 Ottawa, 451 Smyth Rd., Ottawa, ON K1H 8M5, Canada  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Zhou,T.H., Wu,Y.L., Wang,P. and Pei,G.
1 (bases 1 to 1577)
Identification of novel human calcium/calmodulin-dependent protein
kinase II beta subunits
Unpublished
2 (bases 1 to 1577)
Zhou,T.H., Wu,Y.L., Wang,P. and Pei,G.
Direct Submission
Submitted (03-AUG-1998) Max-Planck Guest Lab., Shanghai Institute
of Cell Biology, 320 Yue-Yang Road, Shanghai 200031, China
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1 (bases 1 to 1703)
Li,G., Liu,N., Liu,O.L., Mower,G.D., Gregg,R.G. and Cooper,N.G.
Molecular cloning and analysis of Ca2+/calmodulin-dependent protein
kinase II from the chicken brain
J. Mol. Neurosci. 11 (2), 135-139 (1998)
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PUBMED 10096040
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Li,G.Y. and Cooper,N.G.F.
Direct Submission
Submitted (23-AUG-1998) Anatomical Sciences & Neurobiology,
University of Louisville, 500 S. Preston Street, Louisville, KY
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 REFERENCE 1  
 AUTHORS Rochlitz H., Voigt, A., Lankat-Buttgereit, B., Goetze, B., Heimberg, H., Nauck, M.A., Schiemann, U., Schatz, H. and Pfeiffer, A.  
 TITLE Cloning of the Human Calcium/Calmodulin dependent Protein Kinase II isoforms in human beta cells  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1557)  
 AUTHORS Rochlitz, H.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-DEC-1999) Rochlitz H., Department of Internal Medicine, University Hospital Bergmannsheil, Burkle de la Camp Pl. 1, 44789 Bochum, GERMANY  
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 REFERENCE 1 (bases 1 to 1653)  
 AUTHORS Wu, Y.L., Zhou, T.H., Cen, B. and Pei, G.  
 TITLE Identification of novel human calcium/calmodulin-dependent protein  
 kinase II beta subunits  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1653)  
 AUTHORS Wu, Y.L., Zhou, T.H., Cen, B. and Pei, G.  
 TITLE Direct Submission  
 JOURNAL Submitted (11-AUG-1998) Max-Planck Guest Lab., Shanghai Institute  
 of Cell Biology, 320 Yue-Yang Road, Shanghai 200031, China  
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REFERENCE 1 (bases 1 to 1750)  
AUTHORS Li, G.Y. and Cooper, N.G.F.  
TITLE Molecular cloning and sequencing of human calcium/calmodulin  
dependent protein kinase II beta subunit  
JOURNAL Unpublished  
AUTHORS 2 (bases 1 to 1750)  
Li, G.Y. and Cooper, N.G.F.

TITLE Direct Submission  
JOURNAL Submitted (09-DEC-1998) Anatomical Sciences & Neurobiology,  
University of Louisville, 500 Preston Street, Louisville, KY 40292,  
USA  
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DEFINITION Xenopus laevis calmodulin dependent protein kinase II beta subunit
mRNA, complete cds.
ACCESSION U06636
VERSION U06636.1 GI:1079486
KEYWORDS
SOURCE Xenopus laevis (African clawed frog)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 2508)
AUTHORS Taylor W.L.
TITLE NONE
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2508)
AUTHORS Taylor W.L.
TITLE Direct Submission
JOURNAL Submitted (10-FEB-1994) William L. Taylor, Molecular Physiology and
Biophysics, Vanderbilt University School of Medicine, Light Hall
Room 737, 21st Ave S., Nashville, TN 37232-0615,
USA
COMMENT On Nov 29, 1995 this sequence version replaced gi:466359.
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BASE COUNT 744 a 601 c 596 g 567 t
ORIGIN

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Pred. No.: 1.33e-179 Length: 2508
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DB: 5 Gaps: 1

US-09-820-790B-2 (1-516) x XLU06636 (1-2508)
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RESULT 13
LOCUS HSA252236
DEFINITION Homo sapiens mRNA for calcium/calmodulin dependent protein kinase II beta 1 (CaMK II beta 1 gene).
ACCESSION AJ252236
VERSION AJ252236.1 GI:6688223
KEYWORDS calcium/calmodulin dependent protein kinase II beta 1; CaMK II beta 1 gene.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1

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AUTHORS Rochlitz H., Voigt A., Lankat-Buttgerit B., Goese B., Heimberg H.,
Nauck M.A., Schlemann U., Schatz H. and Pfeiffer A.
TITLE Cloning of the Human Calcium/Calmodulin dependent Protein Kinase II
isoforms in human beta cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1764)
AUTHORS Rochlitz H.
TITLE Direct Submission
JOURNAL Submitted (28-DEC-1999) Rochlitz H., Department of Internal
Medicine, Universityhospital bergmannsheil, Burkle de la Camp Pl.
1, 44789 Bochum, GERMANY
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VERSION BC019070.1 GI:17512172  
KEYWORDS MGC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 1905)  
AUTHORS Strausberg,R.  
TITLE Direct Submission  
JOURNAL Submitted (07-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
  
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov  
COMMENT Contact: MGC Help desk  
Email: cgaps-re@mail.nih.gov  
Tissue Procurement: DCTD/DTP  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland:  
Web site: http://www.nisc.nih.gov/  
Contact: nisc.mgc@nih.gov  
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R., Lim,M., Maduro,Q.L., Masilelo,C., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Snyder,B., Stanttripop,S., Thomas,P.J., Tongson,F.E., Touchman,J.W., Tsurgueon,C., Vogt,J.L., Walker,M.A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 39 Row: 1 Column: 9  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10835005.  
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 Best Local Similarity: 87.82% Mismatches: 1  
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US-09-820-790B-2 (1-516) x BC019070 (1-1905)

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 QY 81 SerGluGluGlyPheHisTyrLeuValPheAspLeuValThrGlyGlyGluLeuPheGlu 100  
 DB 454 TCCGAGGAGGCTTCCACTACCTGGCTTCGATCTGTCATCTGGTGGGAGCTCTTTGAA 513  
 QY 101 AspIleValAlaArgGluTyrTyrSerGluAlaAspAlaSerHisCysIleGlnIle 120  
 DB 514 GACATTTGGCGAGAGATCTACTACAGGAGGCTGTGCTGCTGCTATCTCCAGCAGATC 573  
 QY 121 LeuGluAlaValLeuHisCysHisGlnMetGlyValValHisArgAspLeuLysProGlu 140  
 DB 574 CTGGAGGCGCTTCTCCATTGTCAACAAATGCGGGGTCTGCCACAGACCTCAAGCCGGAG 633  
 QY 141 AsnLeuLeuLeuAlaSerLysCysLysGlyAlaValLysLeuAlaAspPheGlyLeu 160  
 DB 634 AACCTGCTCTCTGGCGAGCAAGTCAAAAGGGGCTGACGTGAAGCTGGCAGACTTCGGCCTA 693  
 QY 161 AlaIleGluValGlnGlyAspGlnGlnAlaTyrPheGlyPheAlaGlnThrProGlyTyr 180  
 DB 694 GCTATCGAGGTGCGAGGGGACACAGAGGATGGTTTGGTTTTCGCTGGCACACCGAGCTAC 753  
 QY 181 LeuSerProGluValLeuArgLysGluAlaTyrGlyLysProValAspIleTyrPalaCys 200  
 DB 754 CTGTCCTCTGAGGTCTCTCCAAAGAGGCGTATGCCAAGCCTGTGGACATCTGGGCATGT 813  
 QY 201 GlyValIleLeuTyrIleLeuLeuValGlyTyrProPheThrAspGluAspGlnHis 220  
 DB 814 GGGGTGATCTCTCATCTCTGCTGGGTACCCACCTCTTCTGGGAGGACACAGCAGC 873  
 QY 221 LysLeuTyrGlnGlnIleLysAlaGlyAlaTyrAspPheProSerProGluTyrAspThr 240  
 DB 874 AAGCTGTACCAGAGATCAGGCTGTGTGCTATGACTTCCCGTCCCTCGAGTGGGACACC 933  
 QY 241 ValThrProGluAlaLysAsnLeuIleAsnGlnMetLeuThrIleAsnProAlaLysArg 260

DB 934 GTCACTCTCTGAGCGCAAAACCTCATCAACAGATGCTGACCATCAACCTGCCAAGGCG 993  
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 QY 301 LysGlyAlaIleLeuThrThrMetLeuAlaThrArgAsnPheSerValGlyArgGlnThr 320  
 DB 1114 AAGGAGCCATCTCCACCATGCTGGCCACAGGAATTTCTCAGCA ----- 1161  
 QY 321 ThrAlaProAlaThrMetSerThrAlaAlaSerGlyThrThrMetGlyLeuValGluGln 340  
 DB 1161 ----- 1161  
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 QY 434 ----- 434  
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 QY 435 PheTyrPheGluAsnLeuLeuAlaLysAsnSerLysProIleHisThrThrIleLeuAsn 454  
 DB 1477 TTCTACTTCGAGAACCCTGTGCCAAGACAGCAAGCCGATCCACAGCAGCATCCTGAC 1536  
 QY 455 ProHisValHisValIleGlyGluAspAlaAlaCysIleAlaTyrIleArgLeuThrGln 474  
 DB 1537 CCACACGTGCACGTCTGAGAGGATGCGGCTGCTGATCGCTTACATCGGCTCACGAG 1596  
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 QY 495 ArgArgAspGlyLysTyrPheGlnAsnValHisPheHisCysSerGlyAlaProValAlaPro 514  
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 DB 1717 CTGCAG 1722

## RESULT 15

XLUI18196 2564 bp mRNA linear VRT 18-DEC-1994  
 LOCUS Xenopus laevis calcium/calmodulin-dependent kinase type II  
 DEFINITION beta'-subunit mRNA, complete cds.  
 ACCESSION U18196  
 VERSION U18196.1 GI:603212  
 KEYWORDS Xenopus laevis (African clawed frog)  
 SOURCE Xenopus laevis  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



QY 459 ValIleGlyGluAspAlaAlaCysIleAlaTyrIleArgLeuThrGlnTyrIleAspGly 478  
 Db 1771 GTAGTGGGAGAGGACGCTGCTGTATCGCTTACATTCGTCAGCGAGTATATCGACACG 1830  
 QY 479 GlnGlyArgProArgThrSerGlnSerGlnGluThrArgValTrpHisArgArgAspGly 498  
 Db 1831 CAGGGGGGGCCCTCGCACCCAGTCAGTCTGAGGAAACCGGTCTGGCATCGTCGTGACGGC 1890  
 QY 499 LysTrpGlnAsnValHisPheHisCysSerGlyAlaProValAlaProLeuGln 516  
 Db 1891 AAATGCGAGATGTGCATTCCACTGTTTCAGGGGGCTCCCGTTGCACCCCTCCAG 1944

Search completed: October 10, 2003, 10:00:45  
 Job time : 5790 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 10, 2003, 03:59:49 ; Search time 8117 Seconds  
(without alignments)  
11178.705 Million cell updates/sec

Title: US-09-820-790b-1

Perfect score: 2218  
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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4: gb.om.\*

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41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1490.4	67.2	1825	9	AF112472 Homo sapi
2	1468	66.2	1727	9	AF078803 Homo sapi
3	1415	63.8	1905	9	BC019070 Homo sapi
4	1402	63.2	1577	9	AF081924 Homo sapi
5	1334	60.1	1840	10	M6112 Rat brain t
6	1330.4	60.0	1750	9	AF112471 Homo sapi
7	1308	59.0	1653	9	AF083419 Homo sapi
8	1304.2	58.8	1557	9	HS252238 Homo sapi
9	1296	58.4	3830	10	MNCAMK2 X63615 M.musculus
10	1291.4	58.2	2220	9	HSU23460 Human proli
11	1288.6	58.1	1764	9	AJ252236 Homo sapi
12	12214	54.7	1610	9	AF081572 Homo sapi
13	1136.2	51.2	1703	5	AF085249 Gallus ga
14	1101.4	49.7	1775	9	HS252237 Homo sapi
15	994.8	44.9	1448	9	AF140350 Homo sapi
16	961.2	43.3	2508	5	XLU06636 Xenopus lae
17	923.4	41.6	1979	10	RNCCDPK2 X83375 R.norvegicus
18	905.8	40.8	2564	5	XLU18196 Xenopus lae
19	886.8	40.0	1941	4	SSU72973 Sus scrofa
20	875.2	39.5	1930	4	AF464186 Mustela p
21	843.4	38.0	3736	9	BC034044 Homo sapi
22	825.8	37.2	1728	10	RATPK2G J04063 Rat calmodu
23	824.2	37.2	1829	4	AF464185 Mustela p
24	818.4	36.9	1829	4	D14905 Oryctolagus
25	814.2	36.7	1793	9	HOMCCDPKB L07044 Homo sapien
26	800.4	36.1	1851	4	SSU72970 Sus scrofa
27	794.4	35.8	1838	4	AF464184 Mustela p
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29	786	35.4	1823	10	AF395884 Mus muscu
30	777	35.0	2696	4	AF464187 Mustela p
31	772.4	34.8	1764	10	S71570 Ca2+/calmod
32	767.6	34.6	1775	4	AF464182 Mustela p
33	762.8	34.4	1757	4	SSU72971 Sus scrofa
34	759.8	34.3	3572	10	BC025597 BC025597 Mus muscu
35	752.6	33.9	1695	10	S71571 S71571 Ca2+/calmod
36	742.2	33.5	1750	5	AF085248 Gallus ga
37	737.2	33.2	1880	6	AX642971 Sequence
38	730	32.9	1495	9	AF145711 Homo sapi
39	722.8	32.6	1732	5	AF109069 Gallus ga
40	722.2	32.6	2021	5	AF233630 Xenopus l
41	721.4	32.5	5637	6	AX401861 Sequence
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43	719.2	32.4	4797	9	AB023185 Homo sapi
44	718.4	32.4	1548	9	AF091486 Homo sapi
45	717.6	32.4	4807	9	BC040457 Homo sapi

## ALIGNMENTS

RESULT 1	AF112472	1825 bp	mRNA	linear	PRI 10-JAN-1999
LOCUS	AF112472				
DEFINITION	Homo sapiens calcium/calmodulin-dependent protein kinase II beta subunit mRNA, complete cds.				
ACCESSION	AF112472				
VERSION	AF112472.1	GI:4139269			
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 1825)				
AUTHORS	Li,G.Y. and Cooper,N.G.F.				
TITLE	Molecular cloning and sequencing of human calcium/calmodulin				

217	QY	CGCCGAGCGGACCGGAGCGGACCGAGCGGTCGCGCGCGCCATGSCCACCACGGTG	276
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277	QY	ACCTGCACCGCGTTCACCGAGGATACCACTCTACGAGGATATTCGCAAGGGCGTTTC	336
62	Db	ACCTGCACCGCGTTCACCGAGGATACCACTCTACGAGGATATTCGCAAGGGCGTTTC	121
337	QY	TTGTGTGCCAGCGCTGTCAAGCTCTGCACCGGCCATGAGTATCAGCCAAAGATCATC	396
122	Db	TTGTGTGCCAGCGTGTCTCAAGCTCTGCACCGGCCATGAGTATCAGCCAAAGATCATC	181
397	QY	AACACCAAGAGCTGTACCCAGAGATCACCAAGCTGTGAGAGAGAGCTCGATCTGC	456
182	Db	AACACCAAGAGCTGTACCCAGAGATCACCAAGCTGTGAGAGAGAGCTCGATCTGC	241
457	QY	CGCCTCTTGAGACGATTCACCAATCGTGGCTCTCCAGACAGCATCTCCGAGGAGGGTTC	516
242	Db	CGCCTCTTGAGACGATTCACCAATCGTGGCTCTCCAGACAGCATCTCCGAGGAGGGTTC	301
517	QY	CACTACCTGGTCTTCGATCTGGTCACTGGTGGGAGCTCTTTGAAGACATATGTGGCGAGA	576
302	Db	CACTACCTGGTCTTCGATCTGGTCACTGGTGGGAGCTCTTTGAAGACATATGTGGCGAGA	361
577	QY	GAGTACTACAGGAGGCTGATCCAGATCACTGTATCCAGAGATCTCTGAGGCGGTTC	636
362	Db	GAGTACTACAGGAGGCTGATCCAGATCACTGTATCCAGAGATCTCTGAGGCGGTTC	421
637	QY	CATTGTACCAAAATGGGGGTCTCCACAGAGACCTCAAGCCGGAGAACTCGTCTCTGGCC	696
422	Db	CATTGTACCAAAATGGGGGTCTCCACAGAGACCTCAAGCCGGAGAACTCGTCTCTGGCC	481
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Db 1562 GCGCGCGCGCCGACCCAGCTCTGAGGAGACCCCGCTGTGGACCGCGCGGAGCGAAG 1621
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Db 1622 TGGCAGAACGTGCACTTCCACATGCTCGGGCGCGCTGTGTGCGCCCGCTGCAGTGAAG 1677

RESULT 2
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LOCUS Homo sapiens calcium/calmodulin-dependent protein kinase II beta
DEFINITION subunit mRNA, complete cds.
ACCESSION AF078803
VERSION AF078803.1 GI:5326756
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1 (bases 1 to 1727)
AUTHORS Zhou, T.H., Wu, Y.L., Ma, L. and Pei, G.
TITLE Identification of novel human Calcium/Calmodulin-dependent protein
kinase II beta subunits
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1727)
AUTHORS Zhou, T.H., Wu, Y.L., Ma, L. and Pei, G.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-1998) Max-Planck Guest Lab., Shanghai Institute
of Cell Biology, #320, Yue-Yang Road, Shanghai 200031, People's
Republic of China
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Location/Qualifiers
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BASE COUNT 404 a 531 c 493 g 309 t
ORIGIN
Query Match 66.2%; Score 1468; DB 9; Length 1727;
Best Local Similarity 95.2%; Pred. No. 6.3e-237;
Matches 1556; Conservative 0; Mismatches 0; Indels 78; Gaps 1;
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Db 1 GCCATGCCACCGGTGACCTGCACCGCTTCACCGACGATACCGATACGATGATGATGATGAT 60
QY 319 ATTGGCAAGGGGGCTTTCTGTGTGTCGACGCTGTCTCAAGCTCTGCACGGGCCATGAG 378
Db 61 ATTGGCAAGGGGGCTTTCTGTGTGTCGACGCTGTCTCAAGCTCTGCACGGGCCATGAG 120
QY 379 TATGAGCCCAAGATCATCAACCAAGAGAGCTGTACGCCAGATCATCAAGAGCTGGAG 438
Db 121 TATGAGCCCAAGATCATCAACCAAGAGAGCTGTACGCCAGATCATCAAGAGCTGGAG 180
QY 439 AGAGAGGCTGGATCTGCGCGCTTCTGAAGCATTCACACATCTGCTGCTCCACGACAGC 498
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Db 181 AGAGAGGCTCGATGTGCGCGCTTCTGAAGCATTCGAACATCGTGGCTTCCACGACAGC 240
QY 499 ATCTCCGAGAGGGGCTTCCACTACCTGCTTCCGATCTGCTGCTGCTGCTGCTGCTGCTGCT 558
Db 241 ATCTCCGAGAGGGGCTTCCACTACCTGCTTCCGATCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 559 GAAGACATTTGTGGCGAGAGAGTACTACAGGAGGCTGATGCCAGTCACTCACTATATCCAGAG 618
Db 301 GAAGACATTTGTGGCGAGAGAGTACTACAGGAGGCTGATGCCAGTCACTCACTATATCCAGAG 360
QY 619 ATCTGTGAGGCGGTTCTCCATTGTCAACAAATGGGGGCTGCTCCACAGAGACCTCAAGCGG 678
Db 361 ATCTGTGAGGCGGTTCTCCATTGTCAACAAATGGGGGCTGCTCCACAGAGACCTCAAGCGG 420
QY 679 GAGAACTGCTTCTGTGGCCAGCAAGTGCAGAGGGCTGCAGTGAAGCTGGCAGACTTCGGGC 738
Db 421 GAGAACTGCTTCTGTGGCCAGCAAGTGCAGAGGGCTGCAGTGAAGCTGGCAGACTTCGGGC 480
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Db 661 CACAAGCTGTACACAGCAGATCAAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
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Db 1081 AAAACACAGTGCAGCGCCACAGCCCGCCCAAGAGGAGCTTCTCTCTGCGCGCTGGAGGCT 1140
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RESULT 3  
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 DEFINITION Homo sapiens, calcium/calmodulin-dependent protein kinase (cam kinase), II beta, clone MGC:29528 IMAGE:5014712, mRNA, complete cds.  
 ACCESSION BLOC19070  
 VERSION BLOC19070.1 GI:17512172  
 KEYWORDS MGC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 1905)  
 Strausberg, R.  
 Direct Submission  
 Submitted (07-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [gcgabs@mail.nih.gov](mailto:gcgabs@mail.nih.gov)  
 Tissue Procurement: DCTD/BTP  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;  
 Web site: <http://www.nisc.nih.gov/>  
 Contact: [nisc.mcgen@ri.nih.gov](mailto:nisc.mcgen@ri.nih.gov)  
 Sherchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.B., Guan, J., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R., Lim, M., Maduro, Q.L., Masello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J., Tongson, E.B., Touchman, J.W., Tsugeon, C., Vogt, J.L., Walker, M.A., Zhang, L.-H. and Green, E.D.  
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ACCESSION	AF081924		
VERSION	AF081924.1	GI:5326761	
KEYWORDS			
SOURCE	Human sapiens (human)		
ORGANISM	Human sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 1577)		
TITLE	Zhou, T.H., Wu, Y.L., Wang, P. and Pei, G.		
JOURNAL	Identification of novel human calcium/calmodulin-dependent protein kinase II beta subunits		
REFERENCE	2 (bases 1 to 1577)		
AUTHORS	Zhou, T.H., Wu, Y.L., Wang, P. and Pei, G.		
TITLE	Direct Submission		
JOURNAL	Submitted (03-AUG-1998) Max-Planck Guest Lab., Shanghai Institute of Cell Biology, 320 Yue-Yang Road, Shanghai 200031, China		
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LOCUS SN201  
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KEYWORDS

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**SOURCE**

SOURCE: ORGANIZATION

ATNENGO

## REFERENCES

**AUTHOR:**  
**ETHEL E.**

**TITLE**

JOURNAL

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Homo sapiens calcium/calmodulin-dependent protein kinase II beta  
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SM Homo sapiens

Eukaryota; Metazoa; Ch

Mammalia; Eutheria; Pr

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Li, G.Y. and Cooper, N.G.

Molecular cloning and dependent protein kinase

Unpublished

Unpublished  
2 (bases 1 to 1750)

2 (bases 1 to 1750)  
S Iij.G.Y. and Cooper, N.G.

LI, G. Y. and COOPER, N. G.

**TITLE** Direct Submission  
**JOURNAL** Submitted (09-DEC-1998) Anatomical Sciences & Neurobiology,  
 University of Louisville, 500 Preston Street, Louisville, KY 40292,  
 USA  
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DB	781	CGCATCAGCCCATGAGGCCCTGAAGCACCCGCTGGTCTGCCAACGCTCCAGGTGAGCA	840
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LOCUS Homo sapiens mRNA for calcium/calmodulin dependent protein kinase

DEFINITION II beta 4 (CamK II beta 4 gene).

ACCESSION AJ252238

VERSION AJ252238.1 GI:6688227

KEYWORDS calcium/calmodulin dependent protein kinase II beta 4; CamK II beta 4 gene.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Nauck, M.A., Schlemann, U., Schatz, H. and Pfeiffer, A.

TITLE Cloning of the Human Calcium/Calmodulin dependent Protein Kinase II isoforms in human beta cells

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1557)

AUTHORS Rochlitz, H.

TITLE Direct Submission

JOURNAL Submitted (28-DEC-1995) Rochlitz H., Department of Internal Medicine, University Hospital Bergmannsheil, Burkle de la Camp pl. 1, 44789 Bochum, GERMANY

FEATURES

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 ACCESSION X63615.1  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 Harbers, K.  
 REFERENCE 1 (bases 1 to 3830)  
 AUTHORS Direct Submission  
 TITLE Submitted (23-DEC-1991) K. Harbers, Heinrich Pette Institut, Martinistr. 52, 2000 Hamburg 20, FRG  
 JOURNAL  
 REFERENCE 2 (bases 1 to 3830)  
 AUTHORS Harbers, K.  
 TITLE Structure, expression, and chromosome location of the gene for the beta subunit of brain-specific Ca2+/calmodulin-dependent protein kinase II identified by transgene integration in an embryonic

lethal mouse mutant  
 Mol. Cell. Biol. 12 (8), 3644-3652 (1992)  
 MEDLINE 92334366  
 PUBMED 1321343  
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 REFERENCE  
 1 (bases 1 to 2220)  
 AUTHORS Leddy,J.J., Salih,M. and Tuana,B.S.  
 TITLE Direct Submission  
 JOURNAL Submitted (24-MAR-1995) John J. Leddy, Pharmacology, University of  
 Ottawa, 451 Smyth Rd., Ottawa, ON K1H 8M5, Canada  
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 AUTHORS Rochlitz H., Voigt A., Lankat-Buttgereit B., Goebel H., Heimberg H.,  
 Nauk M.A., Schlemmer G., Schatz H. and Pfeiffer A.  
 TITLE Cloning of the Human Calcium/Calmodulin dependent Protein Kinase II  
 isoforms in human beta cells  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1764)  
 AUTHORS Rochlitz H.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-DEC-1999) Rochlitz H., Department of Internal  
 Medicine, University Hospital Bergmannsheil, Burkle de la Camp Pl.  
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LOCUS AF081572 Homo sapiens calcium/calmodulin-dependent protein kinase II beta e'

DEFINITION subunit (cAMKB) mRNA, complete cds.

ACCESSION AF081572

VERSION AF081572.1 GI:5326758

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE 1 (bases 1 to 1610)

AUTHORS Wu, Y.L., Zhou, T.H., Yu, Q.M. and Pei, G.

TITLE Identification of novel human calcium/calmodulin-dependent protein kinase II beta subunits

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1610)

AUTHORS Wu, Y.L., Zhou, T.H., Yu, Q.M. and Pei, G.

TITLE Direct Submission

JOURNAL Submitted (02-AUG-1998) Max-Planck Guest Lab., Shanghai Institute of Cell Biology, 320 Yue-yang Road, Shanghai 200031, China

FEATURES

Location/Qualifiers

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## RESULT 13

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LOCUS

DEFINITION

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subunit mRNA, complete cds.

ACCESSION

AF085249

VERSION

AF085249.1

KEYWORDS

Gallus gallus (chicken)

ORGANISM

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

REFERENCE

1 (bases 1 to 1703)

AUTHORS

Li, G., Liu, N., Liu, O. L., Mower, G. D., Gregg, R. G. and Cooper, N. G.

**TITLE** Molecular cloning and analysis of Ca2+/calmodulin-dependent protein kinase II from the chicken brain  
**JOURNAL** J. Mol. Neurosci. 11 (2), 135-139 (1998)  
**MEDLINE** 99195774  
**PUBMED** 10096040  
**REFERENCE** 2 (bases 1 to 1703)  
**AUTHORS** Li, G.Y. and Cooper, N.G.F.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (23-AUG-1998) Anatomical Sciences & Neurobiology, University of Louisville, 500 S. Preston Street, Louisville, KY 40292, USA  
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## RESULT 15

AF140350  
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 DEFINITION Homo sapiens calcium/calmodulin-dependent protein kinase II beta 7  
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 ACCESSION AF140350  
 VERSION AF140350.1 GI:5326855  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1448)  
 AUTHORS Zhou,T.H., Wu,Y.L., Ma,L. and Pei,G.  
 TITLE Identification of novel human calcium/calmodulin-dependent protein  
 kinase II beta subunits  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1448)  
 AUTHORS Zhou,T.H., Wu,Y.L., Ma,L. and Pei,G.  
 TITLE Direct Submission  
 JOURNAL Submitted (04-APR-1999) Max-Planck Guest Lab., Shanghai Institute  
 of Cell Biology, 320 Yue-Yang Road, Shanghai 200031, P.R.China  
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 ORIGIN

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 QY 1099 TCCATGATGCACAGACAGGAGACTGTGGAGTGTCTGAAAAAGTTCAATGCCAGGAGAAAG 1158  
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QY 901 CTCAGGGAGCATCTCTCACACCATGCTGGCCACACGGAATTTCTCAGCCCGGAGAGCAG 960
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Db |||||
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Db |||||
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Search completed: October 10, 2003, 06:30:05  
Job time : 8140 secs

XX  
77

PR 30-MAR-2001; 2001US-0820790.  
XX (PEKE ) PE CORP NY.  
PA (BEAS/) BEASLEY E M.  
XX  
XX  
PI Shao W, Merkulov GV, Di Francesco V;  
XX  
XX WPI; 2003-046806/04.  
DR P-PSDB; AAE30198.  
XX  
XX New peptides related to calcium/calmodulin-dependent protein kinase  
PT subfamily useful for treating disorders associated with abnormal  
PT expression of kinase in fetal brain, testis, lung small cell carcinoma,  
PT uterus adenocarcinoma -  
XX  
XX Claim 4; Fig 1A; 86pp; English.  
XX  
XX The invention relates to new peptides related to calcium/calmodulin-  
CC dependent protein kinase subfamily. The peptides are useful in  
CC substantial and specific assays related to functional information of the  
CC peptide sequences, to raise antibodies or to elicit immune response, as  
CC reagents in assays to determine the levels of protein in biological  
CC fluids and as markers for tissues where the corresponding protein is  
CC expressed. The peptides and antibodies are useful in drug screening  
CC assays, tissue typing and pharmacogenomic analysis. They are also useful  
CC in treating disorders associated with the absence of, inappropriate or  
CC unwanted expression of kinase protein in fetal brain, testis, lung small  
CC cell carcinoma or uterus endometrium adenocarcinoma, such as cancer,  
CC inflammation, immune disorders or disorders affecting growth and  
CC development. The invention is useful as models for the development of  
CC human therapeutic targets, aid in the identification of therapeutic  
CC proteins and serve as targets for the development of human therapeutic  
CC agents that modulate kinase activity in cells and tissues that express  
CC the transporter. The host cells are useful in producing a kinase protein  
CC or peptide and non-human transgenic animals. The invention is useful in  
CC gene therapy. Kinase protein gene is located on chromosome 7. The present  
CC sequence is human kinase protein cDNA.  
XX  
SQ Sequence 2218 BP; 478 A; 727 C; 645 G; 368 T; 0 other;  
Query Match 100.0%; Score 2218; DB 25; Length 2218;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Dd 2161 CATGACCCCTAAAGAGCAAGCCACACCGGCTCTGCTAGCTAGTGTCGCGGCTGTGG 2218

RESULT 2

ABZ23378  
ID ABZ23378 standard; cDNA; 1727 BP.

XX ABZ23378;

DT 07-APR-2003 (first entry)

DE Nucleotide sequence of oestrogen receptor alpha cofactor CF19.

XX Human; oestrogen receptor alpha; ER-alpha; CF16; CF17; CF18; CF19; CF40;  
KW CF41; CF42; CF43; cofactor; osteoporosis; bone disease; reproduction;  
KW hormonal dysfunction; cancer; cardiovascular disease; atherosclerosis;  
KW hot flush; mood change; Alzheimer's disease; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
FT CDS 4..1632  
FT /tag= a  
FT /product= "oestrogen receptor alpha cofactor CF19"

XX WO200270699-A2.

XX 12-SEP-2002.

XX PD

PF 28-FEB-2002; 2002WO-EP02189.  
XX  
PR 01-MAR-2001; 2001EP-0105062.  
XX  
PA (LION-) LION BIOSCIENCE AG.  
XX  
PI Albers M, Ellwanger S, Loeser E, Koegl M;  
XX WPI; 2002-713451/77.  
DR P-PSDB; ABP70158.  
XX  
PT New cofactors of estrogen receptor alpha, designated as CF16, CF17,  
PT CF18, CF19, CF40, CF41, CF42 and/or CF43, useful for screening of  
PT compounds for treating osteoporosis, hormonal dysfunctions, cancer or  
PT cardiovascular diseases -  
XX  
XX Claim 1; Page 74; 111pp; English.  
XX  
CC The present sequence encodes a cofactor of oestrogen receptor alpha  
CC (ER-alpha), designated CF19. The specification describes CF16, CF17,  
CC CF18, CF19, CF40, CF41, CF42, and CF43. The cofactor polypeptides and  
CC nucleic acid molecules are useful for screening for compounds for  
CC treating osteoporosis and other bone diseases, failures in reproductive  
CC functions or hormonal dysfunctions, cancer or cardiovascular diseases  
CC such as atherosclerosis, and in preventing hot flushes, mood changes  
CC and Alzheimer's disease. The CF proteins are also useful for screening  
CC for ligands of the ER alpha. The nucleic acid sequences are useful for  
CC making vectors and CF polypeptides, transforming host cells, as research  
CC tools for developing nucleic acid probes, and for developing analytical  
CC tools such as antisense oligonucleotides.  
XX  
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Query Match 66.2%; Score 1468; DB 24; Length 1727;

Best Local Similarity 95.2%; Pred. No. 6.4e-285;

Matches 1556; Conservative 0; Mismatches 0; Indels 78; Gaps 1;

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QY 319 ATTGGCAAGGGGGCTTTCTCTGTGTCCGACGCTGTGTCAAGCTGTCAACGGCCATGAG 378  
Dd 61 ATTGGCAAGGGGGCTTTCTCTGTGTCCGACGCTGTGTCAAGCTGTCAACGGCCATGAG 420  
QY 379 TATCGACCCCAAGATCATCAACACCAAGAGCTGTCAAGCAGAGATCACCAGAGCTGGAG 438  
Dd 121 TATCGACCCCAAGATCATCAACACCAAGAGCTGTCAAGCAGAGATCACCAGAGCTGGAG 480  
QY 439 AGAGAGGCTCGGATCTGCGGCTTCTGAAGCATTCACATCGTCTCTCCAGACAGC 498  
Dd 181 AGAGAGGCTCGGATCTGCGGCTTCTGAAGCATTCACATCGTCTCTCCAGACAGC 240  
QY 499 ATCTCCGAGAGGGCTTCCACTACCTGCTTGTGTCTGTGTGTGTGTGTGTGTGTGT 558  
Dd 241 ATCTCCGAGAGGGCTTCCACTACCTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 300  
QY 559 GAACACATTTGTGGAGAGAGTACTACAGCGAGGCTGTGAGGAGTCACTGTATCCAGCAG 618  
Dd 301 GAACACATTTGTGGAGAGAGTACTACAGCGAGGCTGTGAGGAGTCACTGTATCCAGCAG 360  
QY 619 ATCTGTGAGGCGCTTCTCCATTGTCAACAAATGGGGTGTCTCCACAGAGACTCAAGCGG 678  
Dd 361 ATCTGTGAGGCGCTTCTCCATTGTCAACAAATGGGGTGTCTCCACAGAGACTCAAGCGG 420  
QY 679 GAGAACTCTGTTGTGGCAGAGAGTGTGAAAGGGGCTGTGAGTGAAGTGTGGAGACTTGGG 738  
Dd 421 GAGAACTCTGTTGTGGCAGAGAGTGTGAAAGGGGCTGTGAGTGAAGTGTGGAGACTTGGG 480  
QY 739 CTAGCTATCGAGTGTGAGGGGACCCAGCAGGCTGTGTTGTTTGTGTTGTTGTTGTTGTT 798  
Dd 481 CTAGCTATCGAGTGTGAGGGGACCCAGCAGGCTGTGTTGTTTGTGTTGTTGTTGTTGTT 540

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QY 799 TACCTGTCCTGAGGTCCTTCGCAAGAGCGGTATGCGAAGCCTGTGGACATCTGGCA 858
Db 541 TACCTGTCCTGAGGTCCTTCGCAAGAGCGGTATGCGAAGCCTGTGGACATCTGGCA 600
QY 859 TGTGGGGTATCCTGTATCATCTCTGCTGCTGGCTACCCACACCTTCTGGGACAGGACAG 918
Db 601 TGTGGGGTATCCTGTATCATCTCTGCTGCTGGCTACCCACACCTTCTGGGACAGGACAG 660
QY 919 CACAAAGCTGTACCAAGCAGATCAAGGCTGTGCTATGACTTCCCGTCCCTGAGTGGAC 978
Db 661 CACAAAGCTGTACCAAGCAGATCAAGGCTGTGCTATGACTTCCCGTCCCTGAGTGGAC 720
QY 979 ACCGTCACTCTGTGAAGCAAAACCTCATCAACAGATGCTGACCATCAACCTGCCAAG 1038
Db 721 ACCGTCACTCTGTGAAGCAAAACCTCATCAACAGATGCTGACCATCAACCTGCCAAG 780
QY 1039 CGCATCACAGCCATGAGGCGCTGAAGCACCGTGGGTCTGCCAACGCTCCACGGTAGCA 1098
Db 781 CGCATCACAGCCATGAGGCGCTGAAGCACCGTGGGTCTGCCAACGCTCCACGGTAGCA 840
QY 1099 TCCATGATGCACAGCAGGAGCTGTGGAGTCTCTAAAAAGTTCAATGCCAGGAAAG 1158
Db 841 TCCATGATGCACAGCAGGAGCTGTGGAGTCTCTGAAAGTTCAATGCCAGGAAAG 900
QY 1159 CTCAGGAGGCATCTCACACATGCTGGCCACACGGAATTTCTAGTGGGCGACAG 1218
Db 901 CTCAGGAGGCATCTCACACATGCTGGCCACACGGAATTTCTAGTGGGCGACAG 960
QY 1219 ACCACCGTCCGGCCACAATGTCCACCGGCGCTCCGCCACACCATGGGCTGTGGAA 1278
Db 961 ACCACCGTCCGGCCACAATGTCCACCGGCGCTCCGCCACACCATGGGCTGTGGAA 1020
QY 1279 CAAGCCAAAGTTTACTCAACAAGAAAGCAGATGGAGTCAAGCCCGACAGCAATAGCAC 1338
Db 1021 CAAGCCAAAGTTTACTCAACAAGAAAGCAGATGGAGTCAAGCCCGACAGCAATAGCAC 1080
QY 1339 AAAACAGTGCAGCGCCACACGCCCCAAAGGAGCGTCTCTCTGCGCGCTGGAGCCT 1398
Db 1081 AAAACAGTGCAGCGCCACACGCCCCAAAGGAGCGTCTCTCTGCGCGCTGGAGCCT 1140
QY 1399 CAAACACCGTCATCATACCCAGTGGAGCGGATTAAGGAGTCTTCTGACAGTGCCAA 1458
Db 1141 CAAACACCGTCATCATACCCAGTGGAGCGGATTAAGGAGTCTTCTGACAGTGCCAA 1200
QY 1459 ACACCATAGAGATGAAGCGCTAAAGCCCGGAAGCAGGAGTATTAGACACCGAG 1518
Db 1201 ACACCATAGAGATGAAGCGCTAAAGCCCGGAAGCAGGAGTATTAGACACCGAG 1260
QY 1519 CAGCTCATGAGCGGCTCAACACGCTGACTTTGAGGCTTACGC----- 1562
Db 1261 CAGCTCATGAGCGGCTCAACACGCTGACTTTGAGGCTTACGC----- 1320
QY 1563 ----- 1562
Db 1321 GGSGTGAOCTGTTGAGCCTGAAGCAGTGGACACTGGGACCTGGTTGAGGGATGACTTCCAC 1380
QY 1563 --ATTCTACTTCGAGAACCTGTGCGCCAAAGAACAGACGAGATCCACAGCACCATCTG 1620
Db 1381 AGATTCTACTTCGAGAACCTGTGCGCCAAAGAACAGACGAGATCCACAGCACCATCTG 1440
QY 1621 AACCCACAGTGCAGCTCATTGAGAGGATGCCGCTGCATCGCTTACATCCGGTCCAG 1680
Db 1441 AACCCACAGTGCAGCTCATTGAGAGGATGCCGCTGCATCGCTTACATCCGGTCCAG 1500
QY 1681 CAGTACATTGAGCGGCGAGGCGCGCCCGCCACAGCAGTCTGAGGAGACCGCGCTGTGG 1740
Db 1501 CAGTACATTGAGCGGCGAGGCGCGCGCCCGCCACAGCAGTCTGAGGAGACCGCGCTGTGG 1560
QY 1741 CACGCGCGGAGCGCAAGTGGCAGAACGTGCATCTTCCACTGCTGGGCGCGCTGTGGCC 1800
Db 1561 CACGCGCGGAGCGCAAGTGGCAGAACGTGCATCTTCCACTGCTGGGCGCGCTGTGGCC 1620
QY 1801 CGCTGCGAGTGAAG 1814
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Db 1621 CGCTGCGAGTGAAG 1634

## RESULT 3

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AB223379/G
ID AB223379 standard; cDNA; 1727 BP.
XX
AC AB223379;
XX
DT 07-APR-2003 (first entry)
XX
DE Reverse complement of oestrogen receptor alpha cofactor CF19 cDNA.
XX
KW Human; oestrogen receptor alpha; ER-alpha; CF16; CF17; CF18; CF19; CF40;
KW CF41; CF42; CF43; cofactor; osteoporosis; bone disease; reproduction;
KW hormonal dysfunction; cancer; cardiovascular disease; atherosclerosis;
KW hot flush; mood change; Alzheimer's disease; ss.
XX
OS Homo sapiens.
XX
PN WO200270699-A2.
XX
PD 12-SEP-2002.
XX
PF 28-FEB-2002; 2002WO-BP02189.
XX
PR 01-MAR-2001; 2001EP-0105062..
XX
PA (LION-) LION BIOSCIENCE AG.
XX
PI Albers M, Ellwanger S, Loeser E, Koegl M;
XX
WPI: 2002-713451/77.
XX
PT New cofactors of estrogen receptor alpha, designated as CF16, CF17,
PT CF18, CF19, CF40, CF41, CF42 and/or CF43, useful for screening of
PT compounds for treating osteoporosis, hormonal dysfunctions, cancer or
PT cardiovascular diseases
XX
PS Claim 1; Page 75-76; 111pp; English.
XX
CC The present sequence represents the reverse complement of cDNA encoding
CC a cofactor of oestrogen receptor alpha (ER-alpha), designated CF19. The
CC specification describes CF16, CF17, CF18, CF19, CF40, CF41, CF42, and
CC CF43. The cofactor polypeptides and nucleic acid molecules are useful
CC for screening for compounds for treating osteoporosis and other bone
CC diseases, failures in reproductive functions or hormonal dysfunctions,
CC cancer or cardiovascular diseases such as atherosclerosis, and in
CC preventing hot flushes, mood changes and Alzheimer's disease. The CF
CC proteins are also useful for screening for ligands of the ER alpha. The
CC nucleic acid sequences are useful for making vectors and CF polypeptides,
CC transforming host cells, as research tools for developing nucleic acid
CC probes, and for developing analytical tools such as antisense
CC oligonucleotides.
XX
SQ Sequence 1727 BP; 309 A; 483 C; 531 G; 404 T; 0 other;
Query Match 66.2%; Score 1458; DB 24; Length 1727;
Best Local Similarity 95.2%; Pred. No. 6.4e-285;
Matches 1556; Conservative 0; Mismatches 0; Indels 78; Gaps 1;
QY 259 GCATGGCCACACCGTGAAGTCTGACCTGACCCGCTTACCGACGAGTACAGCTTACGAGAT 318
Db 1727 GCATGGCCACACCGTGAAGTCTGACCCGCTTACCGACGAGTACAGCTTACGAGAT 1668
QY 319 ATTGGCAAGGGGGCTTTCTCTGTGGTCCGACGCTGTCTGAAGCTGTGACCGGCGCATGAG 378
Db 1667 ATTGGCAAGGGGGCTTTCTCTGTGGTCCGACGCTGTCTGAAGCTGTGACCGGCGCATGAG 1608
QY 379 TATGACGCCAAGATCATCAACACCAAGAGCTGTGACCGAGAGATCACCAGAGCTGGAG 438
Db 1607 TATGACGCCAAGATCATCAACACCAAGAGCTGTGACCGAGAGATCACCAGAGCTGGAG 1548
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PT New human phosphorylation effectors useful for the diagnosis, treatment  
 PT and prevention of proliferative, immune and neuronal disorders -  
 XX Claim 9; Page 132; 142pp; English.  
 XX  
 CC AA246138-246168 encode human phosphorylation effectors (PHSP),  
 CC designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not given  
 CC in the specification). The sequences were isolated from cDNA libraries  
 CC prepared from various human tissues. The PHSP proteins are useful for  
 CC the diagnosis, treatment and prevention of proliferative disorders,  
 CC immune disorders and neuronal disorders. The PHSP proteins form  
 CC pharmaceutical compositions which useful for treating or preventing  
 CC disorders associated with decreased PHSP expression/activity. PHSP  
 CC antagonists are useful for treating or preventing disorders associated  
 CC with increased PHSP expression/activity.  
 XX  
 SQ Sequence 1676 BP; 395 A; 520 C; 466 G; 305 T; 0 other;  
 Query Match 55.3%; Score 1227.6; DB 21; Length 1676;  
 Best Local Similarity 88.0%; Pred. No. 9.8e-237;  
 Matches 1455; Conservative 0; Mismatches 4; Indels 195; Gaps 3;  
 239 CCGCCAGCCGCTCCGCGCGCCAGCCAGCCAGCGTGCCTGCACCCGCTTCACCGAGC 298  
 Db |||||  
 2 CGCCGAGCCGCTCCGCGCGCCAGCCAGCCAGCGTGCCTGCACCCGCTTCACCGAGC 61  
 Qy |||||  
 299 AGTACACGCTCTACGAGGATATGGCAAGGGGGTCTCTGTGTCCAGCGTGTGCA 358  
 Db |||||  
 62 AGTACACGCTCTACGAGGATATGGCAAGGGGGTCTCTGTGTCCAGCGTGTGCA 121  
 Qy |||||  
 359 AGCTGTGACCGGCAATGATAGCAAGCAAGATCAACCAACCAAGAGCTGTGAGCCA 418  
 Db |||||  
 122 AGCTGTGACCGGCAATGATAGCAAGCAAGATCAACCAACCAAGAGCTGTGAGCCA 181  
 Qy |||||  
 419 GAGATCACCAGAGCTGAGAGAGGCTCGGAGCTCGCGCTTCTGAGAGCTTCCACCA 478  
 Db |||||  
 182 GAGATCACCAGAGCTGAGAGAGGCTCGGAGCTCGCGCTTCTGAGAGCTTCCACCA 241  
 Qy |||||  
 479 TCGTGGCTTCCAGACAGATCTCGAGAGGGCTTCCACTACCTGGTCTTCGATCTGG 538  
 Db |||||  
 242 TCGTGGCTTCCAGACAGATCTCGAGAGGGCTTCCACTACCTGGTCTTCGATCTGG 301  
 Qy |||||  
 539 TCACGTGGTGGGAGCTTTGAGACATTTGGGAGAGAGTACTACACGAGGCTGATG 598  
 Db |||||  
 302 TCACGTGGTGGGAGCTTTGAGACATTTGGGAGAGAGTACTACACGAGGCTGATG 361  
 Qy |||||  
 599 CCAGTCACTGTATCCAGACATCTCGAGAGCGCTTCCATTTGCAACAAATGGGGTGC 658  
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 362 CCAGTCACTGTATCCAGACATCTCGAGAGCGCTTCCATTTGCAACAAATGGGGTGC 421  
 Qy |||||  
 659 TCCAGAGAGCTTCAAGCGGAGAACTCTCTTGGGCGCAGCAGTGCAGAGGGCTGAG 718  
 Db |||||  
 422 TCCAGAGAGCTTCAAGCGGAGAACTCTCTTGGGCGCAGCAGTGCAGAGGGCTGAG 481  
 Qy |||||  
 719 TGAAGTGGCAGACTTCGGCTAGCTATCGAGGTGCAAGGGGACCAAGGAGCATGGTTG 778  
 Db |||||  
 482 TGAAGTGGCAGACTTCGGCTAGCTATCGAGGTGCAAGGGGACCAAGGAGCATGGTTG 541  
 Qy |||||  
 779 GTTTCGTGGCAGCACCAGGCTACCTGTCCCTGAGGTCCCTTCGCAAGAGGGCTATGCA 838  
 Db |||||  
 542 GTTTCGTGGCAGCACCAGGCTACCTGTCCCTGAGGTCCCTTCGCAAGAGGGCTATGCA 601  
 Qy |||||  
 839 AGCCTGTGACATCTGGGCTATGCGGTGATCTGTATACCTCTGCTGGGCTACCCAC 898  
 Db |||||  
 602 AGCCTGTGACATCTGGGCTATGCGGTGATCTGTATACCTCTGCTGGGCTACCCAC 661  
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 899 CTTCTTGGGAGGAGCAGCAGCAAGCTGTACAGCAGATCAAGGCTGGTGTGCTATGACT 958  
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 662 CTTCTTGGGAGGAGCAGCAGCAAGCTGTACAGCAGATCAAGGCTGGTGTGCTATGACT 721  
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 959 TCCGCTGCCCTGAGTGGGAGCAGGCTACCTCTTGAAGCAAAACCTCATCAACAGATGC 1018  
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 Db |||||  
 842 GCCAAGCTCCACGGTAGCATCCATGATGACACAGCAGGAGCTGTGGAGTGTCTGAAA 901  
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 1199 ATTCTCAGTGGGCGAGACAGACACCGCTCGCGGCCACAATGTCCACCGCGGCTCCGGCA 1258  
 Db |||||  
 962 ATTCTCAG----- 970  
 Qy |||||  
 1259 CCACCATGGGGCTGGTGGAAAGCAAGCAAGATTTACTCTCAACAAAGAGCAGATGAGTCA 1318  
 Db |||||  
 971 -----CAGCCAAAGAGTTTACTCTCAACAAAGAGCAGATGAGTCA 1009  
 Qy |||||  
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 Db |||||  
 1010 AGCCCCATAGCAATAGCAACCCAAACAGCTGAGCGGCCACCCAGCCGCAAGGAGCGCTTC 1069  
 Qy |||||  
 1379 CTCTCTGCGCGCTGGAGCGCTCAAAACCCGCTCATCTCCATAACCCAGTGTGAGCGGATTAAG 1438  
 Db |||||  
 1070 CTCTCTGCGCGCT-----GG 1084  
 Qy |||||  
 1439 AGTCTTCTGACAGTGCATATACCATAGAGGATGAGAGCTTAAAGCCCGGAGAGCAGG 1498  
 Db |||||  
 1085 AGTCTTCTGACAGTGCATATACCATAGAGGATGAGAGCTTAAAGCCCGGAGAGCAGG 1144  
 Qy |||||  
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 Db |||||  
 1145 AGATCATTAAGACCAAGCAGGAGCTCATCTGAGGCGCTCAACACCGTGTACTTTGAGGCT 1204  
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 1563 -----ATTCTACTTCGAGAACCTGTGCGCAAGAACACACAGC 1600  
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 1265 TTGAAGGAGTGGATCTCCACAGATTCTACTTCGAGAACCTGTGCGCAAGAACACAGC 1324  
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 1601 CGATCCACACAGCACCCTCTGAAACCCACAGCTGCACGTCATTGGAGAGGATGCCGCTGCA 1660  
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 1325 CGATCCACACAGCACCCTCTGAAACCCACAGCTGCACGTCATTGGAGAGGATGCCGCTGCA 1384  
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 1721 CTGAGGAGACCCGCTGTGGCACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1780  
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 1445 CTGAGGAGACCCGCTGTGSCACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1504  
 Qy |||||  
 1781 GTCGGGCGGCGCTGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1814  
 Db |||||  
 1505 GTCGGGCGGCGCTGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1538

RESULT 5  
 AA246160  
 ID AA246160 standard; cDNA; 2110 BP.  
 XX  
 AC AA246160;  
 XX  
 DT 16-MAY-2000 (first entry)  
 XX  
 DE cDNA sequence encoding a human phosphorylation effector PHSP-23.  
 XX  
 KW Human; phosphorylation effector; PHSP; proliferative disorder;



immune disorder; neuronal disorder; ss.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 XX CDS 25..1950  
 XX /tag= a  
 XX /product= "phosphorylation effector"  
 PN WO200006728-A2.  
 XX 10-FEB-2000.  
 XX 28-JUL-1999; 99WO-US17132.  
 XX 28-JUL-1998; 98US-0123494.  
 PR 14-SEP-1998; 98US-0152814.  
 PR 14-OCT-1998; 98US-0173482.  
 PR 03-NOV-1998; 98US-0106889.  
 PR 19-NOV-1998; 98US-0109093.  
 PR 22-DEC-1998; 98US-0113796.  
 PR 12-JAN-1999; 99US-0173482.  
 PR 12-JAN-1999; 99US-0229005.  
 XX (INCY-) INCYTE PHARM INC.  
 XX Hillman JL, Lal P, Tang YT, Corley NC, Guebler KJ, Baughn MR;  
 PI Patterson C, Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;  
 PI Reddy R, Lu DAM, Shih LL;  
 XX WPI; 2000-183125/16.  
 DR P-PSDB; AAY68791.  
 XX  
 PT New human phosphorylation effectors useful for the diagnosis, treatment  
 PT and prevention of proliferative, immune and neuronal disorders -  
 XX  
 XX Claim 9; Page 136; 142pp; English.  
 XX  
 CC AA246138-746168 encode human phosphorylation effectors (PHSP),  
 CC designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not given  
 CC in the specification). The sequences were isolated from cDNA libraries  
 CC prepared from various human tissues. The PHSP proteins are useful for  
 CC the diagnosis, treatment and prevention of proliferative disorders,  
 CC immune disorders and neuronal disorders. The PHSP proteins form  
 CC pharmaceutical compositions which useful for treating or preventing  
 CC disorders associated with decreased PHSP expression/activity. PHSP  
 CC antagonists are useful for treating or preventing disorders associated  
 CC with increased PHSP expression/activity.  
 XX  
 SQ Sequence 2110 BP; 466 A; 688 C; 577 G; 379 T; 0 other;  
 Query Match 49.2%; Score 1091.2; DB 21; Length 2110;  
 Best Local Similarity 92.7%; Pred. No. 2.2e-209;  
 Matches 1187; Conservative 0; Mismatches 18; Indels 75; Gaps 1;  
 QY 239 CGCGAGCGCGTCCGCCGCCATGGCCACCAAGGTGACTGACCGGTTCCACGAG 298  
 Db 2 CGCGAGCGCGTCCGCCGCCATGGCCACCAAGGTGACTGACCGGTTCCACGAG 61  
 QY 299 AGTACCAGCTTACGAGGATATGGCAAGGGGCTTCTCTGTGGTCCGACGCTGTCTCA 358  
 Db 62 AGTACCAGCTTACGAGGATATGGCAAGGGGCTTCTCTGTGGTCCGACGCTGTCTCA 121  
 QY 359 AGCTCTGCACCGGCTCAGTATGCCACCAAGATCATCAACCAAGAGCTGTCAAGCA 418  
 Db 122 AGCTCTGCACCGGCTCAGTATGCCACCAAGATCATCAACCAAGAGCTGTCAAGCA 181  
 QY 419 GAGATCACCAGAGCTGGAGAGAGAGCTCGGATCTCGCGCTTCTGAAGCATTCACA 478  
 Db 182 GAGATCACCAGAGCTGGAGAGAGAGCTCGGATCTCGCGCTTCTGAAGCATTCACA 241  
 QY 479 TCGTGGCTCTCCACGACAGCATCTCCGAGGAGGCTTCCACTACCTGCTTCCGATCG 538  
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Db 242 TCCTGGCTCTCCACGACAGCATCTCCGAGGAGGCTTCCACTACCTGCTCTCGATCTGG 301  
 QY 539 TCACTGGTGGGAGCTCTTTGAAGACATTTGCGGAGAGAGTACTACAGCGAGCTGATG 598  
 Db 302 TCACTGGTGGGAGCTCTTTGAAGACATTTGCGGAGAGAGTACTACAGCGAGCTGATG 361  
 QY 599 CCAGTCACCTGATCCAGCAGATCTGAGGCGCTTCTCCATTTGTCACCAATGGGGTGG 658  
 Db 362 CCAGTCACCTGATCCAGCAGATCTGAGGCGCTTCTCCATTTGTCACCAATGGGGTGG 421  
 QY 659 TCCACAGAGACCTCAAGCCGGAGAACCTGTTGTCGCCAGCAAGTGAAGGGGCTGCA 718  
 Db 422 TCCACAGAGACCTCAAGCCGGAGAACCTGTTGTCGCCAGCAAGTGAAGGGGCTGCA 481  
 QY 719 TGAAGTGGCAGACTTCGGCTAGCTATCAGGTGACGGGGGACAGCAGGCATGTTTG 778  
 Db 482 TGAAGTGGCAGACTTCGGCTAGCTATCAGGTGACGGGGGACAGCAGGCATGTTTG 541  
 QY 779 GTTTCGCTGGCACACAGGCTACCTGTCCTGAGGTCTTTCGCAAGAGGCGTATGGCA 838  
 Db 542 GTTTCGCTGGCACACAGGCTACCTGTCCTGAGGTCTTTCGCAAGAGGCGTATGGCA 601  
 QY 839 AGCCTGTGGACATCTGGGCTATGTTGGGTGATCTCTACATCTGCTGSGGCTACCCAC 898  
 Db 602 AGCCTGTGGACATCTGGGCTATGTTGGGTGATCTCTACATCTGCTGSGGCTACCCAC 661  
 QY 899 CCTTCTGGAGAGAGACAGACAGCTGTACAGCAGATCAAGGCTGGTGGCTATGACT 958  
 Db 662 CCTTCTGGAGAGAGACAGACAGCTGTACAGCAGATCAAGGCTGGTGGCTATGACT 721  
 QY 959 TCCGCTCCCTGAGTGGGACACCGCTCACTCTGAAAGCCAAACCTCATCAACAGATGC 1018  
 Db 722 TCCGCTCCCTGAGTGGGACACCGCTCACTCTGAAAGCCAAACCTCATCAACAGATGC 781  
 QY 1019 TGACCATCAACCTGCCAAGCGCATACAGCCCATGAGGCCCTGAAGCACCCGCTGGTCT 1078  
 Db 782 TGACCATCAACCTGCCAAGCGCATACAGCCCATGAGGCCCTGAAGCACCCGCTGGTCT 841  
 QY 1079 GCCAAGCTCCACGGTAGCATTCATGATGCACAGACAGAGACTGTGAGTGTGATAA 1138  
 Db 842 GCCAAGCTCCACGGTAGCATTCATGATGCACAGACAGAGACTGTGAGTGTGATAA 901  
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 Db 902 AGTTCAATGCAGGAGAAAGTCAAGGAGCCATCTCACCACCATGCTGGCCACACGGA 961  
 QY 1199 ATTTCTCAGTGGGACAGACACACCGCTCCGCCCAATGTCCACCCGCGCTCCGGCA 1258  
 Db 962 ATTTCTC----- 968  
 QY 1259 CCACCATGGGCTGGTGGGAACAGCCAAAGAGTTTACTCAACAGAAAGCAGATGGATCA 1318  
 Db 969 -----AGCCAAAGAGTTTACTCAACAGAAAGCAGATGGATCA 1006  
 QY 1319 AGCCCCAGACGAATAGCAACCAAGTGCAGCCGCCACCAAGCCCAAGAGGACGCTTC 1378  
 Db 1007 AGCCCCAGACGAATAGCAACCAAGTGCAGCCGCCACCAAGCCCAAGAGGACGCTTC 1066  
 QY 1379 CTCTGCGCGCTTGGAGCCTCAAAACCCGCTCATCAATCAACCCAGTGGAGGATTAAG 1438  
 Db 1067 CTCTGCGCGCTTGGAGCCTCAAAACCCGCTCATCAATCAACCCAGTGGAGGATTAAG 1126  
 QY 1439 AGTCTCTCAGAGTGGCAATACCAACCATAGAGATGAGAGCTAAAGCCCGGAGCAGG 1498  
 Db 1127 AGTCTCTCAGAGTGGCAATACCAACCATAGAGATGAGAGCTAAAGCCCGGAGCAGG 1186  
 QY 1499 AGATCATTAAGACACCGAG 1518  
 || || || || ||  
 Db 1187 CCGACATCTGAGCTCAGTG 1206





Db 487 GCTGATTTGGCCCTAGCCATCGAAGTACAGGAGAGCAGCGCTGGTTGGTTTGGTTTGGCT 546  
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 QY 1087 TCCAGGTGATCCTCATGATGACAGCAGAGACTGTGGAGTGTCTGAAAAGTTCAAT 1146  
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 QY 1501 ATCATTAAGACCGAGAGAGCTCATCGAGGCGCTCAACAACGGTGACTTTTGAGGCTTAC 1560  
 Db 1267 GGCCTCACTCTTTGAGCTGAGGCGCTTGTGTAACCTCGTGGAGGGGATGATTTCAAT 1326  
 QY 1561 GCATTTCTACTGAGAACCTGTGTCGCAAGACAGCAGCAGCGATCCACAGCACCATCTG 1620  
 Db 1327 AAGTTTACTTTGAGATCTCTCTGTCCAAGACAGCAGGCTATCCATACCACCATCTA 1386  
 QY 1621 AACCCACAGTGCACGTCATTTGAGGAGGATGCCGCTGCTATCTACATCGGCTCAG 1680  
 Db 1387 AACCCACAGTGCACGTCATTTGAGGAGGATGCCGCTGCTATCTACATCGGCTCAG 1446  
 QY 1681 CAGTATTTAGCGGCGAGGCGCGCCCGCCAGCAGTCTGAGGAGCAGCCGCTGTGG 1740  
 Db 1447 CAGTATCTGAGCGGAGGCTGGCTTCGACCCAGCAGCAGTCAAGAGAGACCCGCTGTG 1506  
 QY 1741 CACCGCGGAGCAGAGTGGCAGAAAGTGCATTTCCATCTCTCGGCGCGCTGTGGCC 1800  
 Db 1507 CACCGTGGGATGCAAGTGGCTCAATGTCCACTCATCTGCTCAGGCGCCCTTCGCGCA 1566  
 QY 1801 CGCTGCTGAGTGAACCA 1817  
 |||||

Db 1567 CCGCTCCAGTGAGCTCA 1583  
 RESULT 8  
 AAH99755  
 ID AAH99755 standard; cDNA; 3015 BP.  
 XX AC AAH99755;  
 XX DF 16-OCT-2001 (first entry)  
 XX DE Human protein encoding cDNA sequence SEQ ID NO:590.  
 XX KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;  
 KW antiinflammatory; antihemagic; antiarthritic; immunosuppressive;  
 KW antibacterial; endocrine; cardiant; central nervous system; virucide;  
 KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;  
 KW antiaggregant; haemostatic; vulnery; antiulcer; osteopathic; eczema;  
 KW dermatologic; antiallergic; antidiabetic; antidiabetic; cytostatic;  
 KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;  
 KW immunostimulant; gene therapy; antitense therapy; vaccine; inflammation;  
 KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;  
 KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;  
 KW genetic disease; haematopoietic disorder; platelet disorder; asthma;  
 KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;  
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;  
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;  
 KW neurological disorder; ss.  
 XX OS Homo sapiens.  
 XX PN W0200153455-A2.  
 XX PD 26-JUL-2001.  
 XX PF 22-DEC-2000; 2000WO-US35017.  
 XX PR 23-DEC-1999; 99US-0471275.  
 PR 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-0552317.  
 XX (HYSE-) HYSEQ INC.  
 XX Tang YT, Liu C, Drmanac RT;  
 WPI: 2001-457603/49.  
 P-PSDB; AM25814.  
 XX Isolated human polynucleotides encoding polypeptides, useful for the  
 treatment and diagnosis of e.g. cancer, ulcers and HIV infection -  
 Claim 1; Page 628-629; 1217pp; English.  
 XX AH99166 to AAH99904 encode the human proteins given in AM25225 to  
 AM25963. The proteins can have activities based on the tissues and  
 cells they are expressed in, such as: antiinflammatory; antirheumatic;  
 antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;  
 central nervous system; virucide; anti-HIV; fungicide; antimutagen;  
 cardiovascular; antianaemic; antiaggregant; haemostatic; vulnery;  
 antiulcer; osteopathic; dermatologic; antiallergic; antiasthmatic;  
 antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;  
 antiparkinsonian; and immunostimulant. The proteins and polynucleotides  
 encoding them can be used in gene therapy, antisense therapy and vaccine  
 production. The proteins and polynucleotides are useful for screening for  
 agonists or antagonists of a protein and for the treatment and diagnosis  
 of disorders associated with the activity of a protein e.g. inflammation,  
 rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,  
 neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal  
 infections, autoimmunity, genetic diseases, haematopoietic disorders,  
 anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,  
 osteoporosis, severe combined immunodeficiency, eczema, allergic  
 rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,  
 Alzheimer's disease, Parkinson's disease, neurodegenerative and





RESULT 10  
 ABX63227  
 ID ABX63227 standard; cDNA; 3705 BP.  
 XX AC  
 XX AC ABX63227;  
 XX AC  
 DT 25-FEB-2003 (first entry)  
 XX XX  
 DE Human cDNA #227 differentially expressed in activated vascular tissue.  
 XX XX  
 KW Human; gene; ss; vascular tissue; cytostatic; atherosclerosis;  
 KW cardiant; hypotensive; antidiabetic; gynaecological; vasotropic;  
 KW cerebroprotective; gene therapy; vascular disease; cancer; coronary;  
 KW artery disease; hypertension; diabetes; pre-eclampsia; restenosis;  
 KW ischaemia-reperfusion injury; stroke;  
 XX XX  
 OS Homo sapiens.  
 XX OS  
 PN US2002137081-A1.  
 XX PN  
 PD 26-SEP-2002.  
 XX PD  
 PF 08-JAN-2002; 2002US-0044090.  
 XX PF  
 PR 28-JUL-2000; 2000US-222469P.  
 XX PR  
 FR 08-JAN-2001; 2001US-260483P.  
 XX FR  
 PA (BAND/) BANDMAN O.  
 XX PA  
 PI Bandman O;  
 XX PI  
 XX XX  
 DR WP1; 2003-110597/10.  
 XX DR  
 PT Combination for diagnosing, staging, treating, or monitoring the  
 PT progression of treatment of a vascular disease, e.g. atherosclerosis,  
 PT comprises several cDNAs that are differentially expressed in activated  
 PT vascular tissue -  
 XX PT  
 XX Claim 1; Page -; 18pp; English.  
 XX XX  
 PS This invention relates to a combination comprising several cDNAs that  
 CC are differentially expressed in activated vascular tissue. The invention  
 CC also discloses a high throughput method for detecting differentially  
 CC expressed cDNAs in a sample. The cDNAs of the invention may have  
 CC antiatherosclerotic; cytostatic; cardiant; hypotensive; antidiabetic;  
 CC gynaecological; vasotropic and cerebroprotective activities and may be  
 CC used in gene therapy. The cDNAs of the invention may be used in a  
 CC high-throughput methods for detecting differential expression of one or  
 CC more cDNAs in a sample, or screening several molecules or compounds to  
 CC identify a molecule or compound that specifically binds a cDNA of the  
 CC invention. A protein encoded by the cDNA may be used to screen several  
 CC molecules or compounds to identify a ligand that specifically binds to  
 CC the protein, or to produce or purify an antibody to the protein that c  
 CC be used to detect a protein in a sample or purify a natural or  
 CC recombinant protein from a sample. The nucleotides may be useful for  
 CC diagnosing, staging, treating, or monitoring the progression of  
 CC treatment of a vascular disease, e.g. atherosclerosis, cancer, coronary  
 CC artery disease, hypertension, diabetes, pre-eclampsia, ischaemia-  
 CC reperfusion injury, restenosis, or stroke. The cDNAs can also be used  
 CC for large-scale genetic or gene expression analysis of several new  
 CC nucleic acid molecules. Antibodies to the proteins encoded by the  
 CC cDNAs are useful for diagnosing pre-pathologic disorders, and chronic  
 CC or acute diseases associated with abnormalities in the expression,  
 CC amount or distribution of the protein. The present sequence  
 CC represents a cDNA of the invention that is differentially expressed in  
 CC activated vascular tissue.  
 CC Note: The sequence data for this patent did not form part of the  
 CC specification, but was obtained in electronic format directly from USF  
 CC at <http://seqdata.uspto.gov/sequence.html?docID=20020137081>.  
 XX CC  
 SQ Sequence 3705 BP; 901 A; 961 C; 870 G; 873 T; 0 other;



Db 1029 CTGCCAAA-----AGCCTATTGAACAAGAGTCGGATGSC-----G 1064  
 QY 1268 GCGTGGTGGACCAAGCAAGCTTTACTACACAGAAAGCAGATGGAGTCAAGCCCAAGA 1327  
 Db 1065 GTGTCAAGAGGCCAACAACCACTGTGTGTACACAGCGCTACAGATGGGATCAAGGCTCCA 1124  
 QY 1328 CGAATAGCACCACCAAGAGTGCAGCGCCACCAGCCCAAGAGGAGCGCTTCCTCTCGCG 1387  
 Db 1125 CAGAGAGCTGCAACACCAACAGAGATGAGGACCTCAAGTGCAGAAAC----- 1175  
 QY 1388 CCTGGAGCCTCAACACACCGCTCATCCATFAACCCAGTGGAGCGGATTAAGGATCTTCTG 1447  
 Db 1176 -----AGGAGATCATTAAGATTACAGAAACAGCTGATTGAAGCCATCAACAATGGGACT 1229  
 QY 1448 ACAGTGCCTAATACCAACAGATGAGATGAAGAGCTTAAGCCCGAGAGGAGATCAATA 1507  
 Db 1230 TTGAGGCCATACAGAGATTGTGATCCAGGCTTCCTCTTTGAGCGCTGAGGCCCTTG 1289  
 QY 1508 AGACACGAGCAGCTCATCGAGCGGTCAACAACAGGTGACTTTGAGGCTACGCAATCT 1567  
 Db 1290 GTAACTCTGTGAGGGATGGATTTCATAAG-----TTTT 1325  
 QY 1568 ACTTGAGAACTCTGCTGGCCAGACAGACAGCCGATCCACAGACCATCTGTAACCCAC 1627  
 Db 1326 ACTTTGAGAACTCTGCTGCAAGACAGCAAGCCTATCCATACCAACCTCTTAACCCAC 1385  
 QY 1628 AGTGCACGCTCATTTGAGAGGATGCGCCTGCTGATCTTACATCCGGCTCAGCCAGTACA 1687  
 Db 1386 AGTCCAGTGTGAGGAGGAGCAGCGCTGATCGCTACATCCGCTCACCCAGTACA 1445  
 QY 1688 TTGAGGGCAGGGCGGCCCGCAGCAGCAGCTGTGAGGAGACCGCGGTGTGGACCGCC 1747  
 Db 1446 TCGAGGGCAGGGTGGCCCTCGCAGCAGCAGTCAAGAGACCGCGGCTGTGGACCGTC 1505  
 QY 1748 GCGAGCGCAAGTGGCAGAGCTGCTCTCCACTGTGCGGCGGCTGTGGCGCCGCTGCG 1807  
 Db 1506 GGGATGGCAATGGCTCAATGTCCATATCACTGCTCAGGGGCCCTGCGCACCGCTGC 1565  
 QY 1808 AGTGAAGCA 1817  
 Db 1566 AGTGAGCTCA 1575

RESULT 11

AD39316  
 ID AD39316 standard; cDNA; 2061 BP.

AC AD39316;

DT 22-OCT-2002 (first entry)

DE Human calcium/calmodulin-dependent protein kinase cDNA.

KW Human; calcium/calmodulin-dependent protein kinase; enzyme; inflammation;  
 breast cancer; skin melanoma; adenocarcinoma; arteriosclerosis;  
 Burkitt's lymphoma; uterine leiomyosarcoma; foetal brain tumour; vaccine;  
 psoriasis; gene therapy; protein therapy; cytostatic; antiinflammatory;  
 antiarteriosclerotic; gene; chromosome 10; ss.

OS Homo sapiens.

PH key Location/Qualifiers

FT 5'UTR 1..112

FT \*tag= a

FT CDS 113..1810

FT \*tag= b

FT /product= "Human calcium/calmodulin-dependent

FT protein kinase"

FT 1811..2061

FT \*tag= c

FT 3'UTR

FT US6387677-B1.

PN

XX 14-MAY-2002.  
 PD 08-MAR-2001; 2001US-0800960.  
 XX 08-MAR-2001; 2001US-0800960.  
 PR (PEKE ) PE CORP NY.  
 PA Ye J, Yan C, Di Francesco V, Beasley EM;  
 PI WPI; 2002-478444/51.  
 XX P-PSOB; AAE24635.  
 DR Nucleic acid molecules encoding calcium/calmodulin-dependent protein  
 PT kinases, useful for preventing diagnosing and treating e.g. cancers,  
 PT psoriasis and inflammation -  
 XX Claim 1; Fig 1A; 85pp; English.  
 PS The present invention relates to calcium/calmodulin-dependent protein  
 CC kinases and polynucleotides encoding such proteins. Sequences of the  
 CC invention are used as models for the development of human therapeutic  
 CC targets, aid in the identification of therapeutic proteins and serve  
 CC as targets for the development of human therapeutic agents that modulate  
 CC kinase activity in cells and tissues that express the kinase. They are  
 CC expressed in humans in the placenta, skin melanotic melanomas, breast  
 CC cancers (including mammary adenocarcinoma), duodenal adenocarcinomas  
 CC (small intestine), ovary adenocarcinomas, Burkitt's lymphomas (lymph),  
 CC uterine leiomyosarcomas, foetal brain tumours and in disease conditions  
 CC including inflammation, arteriosclerosis and psoriasis. Sequences of  
 CC the invention are used in gene therapy and protein therapy. They are  
 CC also used as vaccines. The present sequence is human calcium/calmodulin-  
 CC dependent protein kinase cDNA. Calcium/calmodulin-dependent protein  
 CC kinase genomic DNA is located on chromosome 10.  
 XX Sequence 2061 BP; 503 A; 502 C; 547 G; 409 T; 0 other;  
 SQ

Query Match 34.7%; Score 769.4; DB 24; Length 2061;

Best Local Similarity 67.9%; Pred. No. 7.1e-145;

Matches 1233; Conservative 0; Mismatches 421; Indels 161; Gaps 5;

QY 159 CTCGCCGCCGCCGCCGCTGTCGCCGCCGCTGCGCCGAGCGGGAGCGCGGAGTCGCCGCCG 218  
 Db 6 CTCGCCGCCGCCGCCGCTGTCGCCGCCGCTGCGCCGAGCGGGAGCGCGGAGTCGCCGCCG 65  
 QY 219 CCGGAGCGCAGCG 274  
 Db 66 ACGGAGCGTGGCGGGCGTGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 125  
 QY 275 TGACCTGCACCCCGCTTCCCGAGAGTACAGCTCTACGAGGATATGTCAGAGGGGGCTT 334  
 Db 126 CCACCTGCACCCCGCTTCCCGAGAGTACAGCTCTTCCGAGGAGCTTGGCAGGGGGCTT 185  
 QY 335 TCTCTGTGTCGCGCGCTGTGTCAAGCTCTGCACCGCGCGCGCGCGCGCGCGCGCGCG 394  
 Db 186 TCTCTGTGTCGCGCGCTGTGTGAAGAAACCTCCACGAGGAGTACGCGCAAAATCA 245  
 QY 395 TCAACACCAAGAACTGTCTGCGCGGATCACCAGAACTAGAACTGAGGCTCGGATCT 454  
 Db 246 TCAATACCAAGAAATGTCTGCGCGGATCACCAGAACTAGAACTGAGGCTCGGATAT 305  
 QY 455 GCGGCTTCTGAAGCATTCACATCGCTGCTCCACGACAGCATCTCCGAGGAGGGCT 514  
 Db 306 GTCGACTTCTGAAGCATTCACATCGCTGCTCCACGACAGCATCTTCTGAAGAGGGT 365  
 QY 515 TCCACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 574  
 Db 366 TTCACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 425  
 QY 575 GAGACTACTACAGCGAGGCTGATGCCAGTCACTGTATCCAGCAGATCTCTGAGCGCGTTC 634  
 Db 426 GAGACTACTACAGTGAAGCAGATGCCAGCCTGTATATCATCATCATCTGAGAGATGTTA 485

QY 635 TCATTTGTCACAAATGGGGCTCGTCCACAGACCTCAAGCCGGAGAACTCTCTCTGG 594  
 DB 486 ACCACATCCACCATGACATCTCCACAGGACCTGAAGCCTGAGAACCTCTCTCTGG 545  
 QY 695 CCACAGTGCAGAGGGCTCGAGTGAAGCTGGCAGACTTGGCCTAGCTATGAGGTGC 754  
 DB 546 CGAGTAATGCAAGGGTCCCGCTCAAGCTGGCTGATTTGGCCTAGCCATCGAAGTAC 505  
 QY 755 AGGGAGCAGCAGAGCATGGTTGGTTGCTGGCAGACACAGGCTTACCTGTCCTCGAGG 814  
 DB 606 AGGAGAGCAGCAGGCTGGTTGGTTGCTGGCAGCACCAGGTTACTTGTCCCTCGAGG 665  
 QY 815 TCCTTCGCAAGAGGCGCTATGGCAAGCCTGTGGACATCTGGGCATGTGGGTGATCTCTG 874  
 DB 666 TCTTGGAGAAATCCCTATGGAACCTGTGGATATCTGGGCTTGGGGGTCTATCTCTG 725  
 QY 875 ACATCTCTGCTCGTGGGCTACCCACCTTCCTGGGACAGGACCCAGCAAGCTGTACGACG 934  
 DB 726 ATATCTCTGCTGGGCTATCTCTCTCTGGATGAGGATCAGCACAAGCTGTATCAGC 785  
 QY 935 AGATCAAGGCTGGTGCCTATGACTTCCGCTCCCTCGAGTGGGACACCGCTCACTCTCGAAG 994  
 DB 786 AGATCAAGGCTGGGCTATGATTCCCATCACCAGATGGCAGCAGTAACTCCTCGAAG 845  
 QY 995 CCAAAAACCTCATCAACAGATGCTGACCATCAACCTGCCAAGGCGATCACAGCCCATG 1054  
 DB 846 CCAAGACTGTATCAACAGATGCTGACCATCAACCTGCCAAGGCGATCACAGGCTGAC 905  
 QY 1055 AGGCGCTGAAGCACCCTGGTGTCTGCCACGCTCCACGCTAGCATCCATGATCACAGAC 1114  
 DB 906 AGGCTCTCAAGCACCCTGGTGTCTGCCACGCTCCACGCTAGCATCCATGATCGTC 965  
 QY 1115 AGAGACTGTGAGTGTCTGAAAAGTTCAATCCAGGAGAAAGCTCAAGGGAGCATCC 1174  
 DB 966 AGGAGACTGTGAGTGTCTGCGCAAGTCAATCCCGGGAGAAAAGTGAAGGGTGCATCC 1025  
 QY 1175 TCACCACTATGTGCGCACACAGAAATTTCTAGTGGGACAGACACACCGCTCCGGCCA 1234  
 DB 1026 TCAGGACCATGTTCTCTCCAGGACTTCTAGTGGGACGAGAGCTCCGCCCGGCT 1085  
 QY 1235 CAATGTCCACCGCGGCTCCCGC----- 1257  
 DB 1086 CGCTGCGGAGCGCGCGGCTCGCGGCAAGCTGCCAAAAGCTATGAACAAGA 1145  
 QY 1258 -----ACCACTATGGGCTGTGGACAG 1282  
 DB 1146 AGTCGGATGGCGGTGTCAAGAAAAGGAAGTCCAGGTTCCAGCGTGCACCTAATGGAGCCAC 1205  
 QY 1283 CCAAGAGTTTACTCAACAAGAAAAGCAGATGGATGAGTCAAGCCCGCAGACGAATAGCAAAA 1342  
 DB 1206 AACCCTGTGGTACACACGCTACAGATGGATCAAGGGCTCCACAGAGAGTGCACA 1265  
 QY 1343 ACAGTGCAGCGCCACAGCCCGCCAAAAGGACGCTTCTCTCGCGCGCTGGAGCCTCAA 1402  
 DB 1266 CCACACAGAAGTGAAGACCTCAA-----GCTGCCCGCTCCGCACTGGGAATGGCAG 1320  
 QY 1403 CCACGCTCATCAACCCAGTGGAGCGGATTAAGAGTCTTTCAGACAGTGCCTATACCA 1462  
 DB 1321 CTCGGTCCCTGAGAGCGGAGTCCCGGAGACGAACAGCCCTCTGAGGAGATGAGCC 1380  
 QY 1463 CCATAGAGTGAAGACGCTAAAGC--CCGGAAGCAGGAGATCATTAAGACCGAGGAGA 1520  
 DB 1381 CCAGCCTCTCTCTCTCTCTAGCCATGCGAAACAGGAGATCATTAAGATTACAGACA 1440  
 QY 1521 GCTCATGAGCGGCTCAACACAGGTGACTTTGAGGCTTACG----- 1562  
 DB 1441 GCTGATTGAAGCCATCAACAATGGGAGCTTTGAGGCTACACGAAGATTGTGATCCAGG 1500  
 QY 1563 ----- 1562  
 DB 1501 CCTCATTCTTTGAGCCTGAGGCCCTTGTTGAACCTCGTGGAGGGATGGATTTCATATA 1560

QY 1563 ATTCTACTTCGAGAACCTGCTGCCAAGACACAGAGCGATCCACAGACCTCTGAA 1622  
 DB 1561 GTTTTACTTTGAGATCTCTCTGTCCTCAAGAACAGAGCCTATCCATACCCATCTATA 1620  
 QY 1623 CCACACGCTGCACGCTCATTTGGAGAGGATGCGCTGCTGATCGCTTACATCGGCTCACGA 1682  
 DB 1621 CCACACGCTGCACGCTCATTTGGAGAGGATGCGCTGCTGATCGCTTACATCGGCTCACGA 1680  
 QY 1683 GTACATTCAGCGGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1742  
 DB 1681 GTACATTCAGCGGCGAGGCTCGGCTCGCACCGACCGAGTCAAGAGAGCGCGGCTGGA 1740  
 QY 1743 CCSCCGGAGCGAGTGGCAGAGACGCTTCCACTGCTCGGCGCGCGCGCGCGCGCGCG 1802  
 DB 1741 CCCTGGGATGGCAAGTGGCTCAATGTCCACTATCTCTCAGGGCGCGCGCGCGCG 1800  
 QY 1803 GCTCAGTGAAGCCA 1817  
 DB 1801 GCTCAGTGAAGTCA 1815

RESULT 12  
 ABX10915  
 ID ABX10915 standard; cDNA; 2061 BP.  
 XX  
 AC ABX10915;  
 XX  
 DT 02-MAY-2003 (first entry)  
 XX  
 DE cDNA encoding novel human kinase.  
 XX  
 KW Human; calcium/calmodulin-dependent protein kinase subfamily;  
 KW kinase; cancer; inflammation; arteriosclerosis; psoriasis;  
 KW mammary adenocarcinoma; skin melanotic melanoma; ovary adenocarcinoma;  
 KW uterus leiomyosarcoma; Burkitt's lymphoma; duodenal adenocarcinoma;  
 KW gene; ss; chromosome 10.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Key  
 FT 5'UTR 1..112  
 FT /\*tag= a  
 FT 113..1810  
 FT /\*tag= b  
 FT /product= "Novel human kinase"  
 FT /notes= "Member of the calcium/calmodulin-dependent  
 FT protein kinase subfamily"  
 FT 3'UTR 1811..2061  
 FT /\*tag= c  
 XX  
 US2002132325-A1.  
 XX  
 PD 19-SEP-2002.  
 XX  
 PF 14-MAR-2002; 2002US-0096960.  
 XX  
 PR 08-MAR-2001; 2001US-0800960.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Ye J, Yan C, Di Francesco V, Beasley EM;  
 XX  
 DR WPI: 2003-247084/24.  
 DR P-PSDB; ABG75873.  
 XX  
 PT New human kinase peptide, useful for preparing a composition for  
 PT treating a disease or condition mediated by a human enzyme protein e.g.  
 PT cancer  
 XX  
 PS Claim 4; Fig 1; 89pp; English.  
 XX  
 CC The invention describes a new isolated peptide (I) comprising a 565  
 CC amino acid sequence or its allelic variant, orthologue or fragment.



QY	1803	GCTGCAGTGAAGCCA	1817	CC	atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,
DB	1801	GCTGCAGTGAAGTCA	1815	CC	autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes
RESULT 13				CC	mellitus, multiple sclerosis, good pasture's syndrome, Graves' disease,
AD26469				CC	osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,
ID	AA26469	standard; cDNA; 1880 BP.		CC	rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,
XX	AC	AA26469;		CC	bacterial, parasitic, fungal, viral, protozoal and helminthic infections)
XX	DT	26-MAR-2002 (first entry)		CC	growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,
XX	DE	Human kinase PKIN-22 cDNA.		CC	Cushing's syndrome, hypothyroidism, cerebral palsy, myocarditis,
XX	XX	Human; kinase; PKIN-22; cancer; leukaemia; adenocarcinoma; osteoporosis;		CC	vascular disease (arteriovenous fistula, hypertension, vasculitis,
KW	KW	immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;		CC	aneurysms, congestive heart failure, angina pectoris, myocarditis,
KW	KW	Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;		CC	disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,
KW	KW	allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;		CC	hypocholesterolaemia, obesity). PKIN DNA is useful for assessing
KW	KW	autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis;		CC	toxicity of a test compound and in gene therapy. The present sequence
KW	KW	Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;		CC	is human PKIN-22 cDNA. Human PKIN-22 gene is located on chromosome 10.
KW	KW	rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;		XX	
KW	KW	hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;		XX	Sequence 1880 BP; 454 A; 558 C; 505 G; 363 T; 0 other;
KW	KW	cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;			Query Match 33.2%; Score 737.2; DB 24; Length 1880;
KW	KW	congestive heart failure; ischaemic heart disease; lung tumour; gout;			Best Local Similarity 67.4%; Pred. No. 2e-138;
KW	KW	fatty liver; Niemann-Pick's disease; gene therapy; chromosome 10; ss.			Matches 1245; Conservative 0; Mismatches 383; Indels 218; Gaps 6;
OS	Homo sapiens.				
XX	Key	Location/Qualifiers			
FT	CDS	83..1849			
FT		/*tag= a			
FT		/product= "Human PKIN-22 protein"			
XX	WO200196547-A2.				
XX	20-DEC-2001.				
XX	14-JUN-2001; 2001WO-US19444.				
XX	15-JUN-2000; 2000US-212073P.				
PR	23-JUN-2000; 2000US-213467P.				
PR	30-JUN-2000; 2000US-215651P.				
PR	07-JUL-2000; 2000US-216605P.				
PR	13-JUL-2000; 2000US-218372P.				
PR	25-AUG-2000; 2000US-228056P.				
XX	(INCY-) INCYTE GENOMICS INC.				
XX	Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y;				
PI	Gandhi AR, Tribouley CM, Walia NK, Yao MG, Lu DM, Greenwald SR;				
PI	Rankumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT;				
PI	Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;				
PI	Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L;				
PI	Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;				
XX	WPI; 2002-090207/12.				
DR	P-PSDB; AAE16276.				
XX	New polypeptides, useful for diagnosing, treating or preventing				
PT	disorders of growth and development, cardiovascular and lipid, and				
PT	diseases such as cancer, comprise human kinase polypeptides -				
XX	Claim 5; Page 193; 197pp; English.				
XX	The invention relates to human kinase PKIN proteins and their				
CC	corresponding cDNAs. A composition containing PKIN agonist is useful for				
CC	treating a disease or condition associated with decreased expression of				
CC	PKIN and a composition comprising PKIN antagonist is useful for treating				
CC	a disease or condition associated with overexpression of PKIN. The				
CC	disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,				
CC	myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder				
CC	(Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,				



KW food additive; food preservative; gene therapy; gene; ss.

XX OS Homo sapiens.  
XX PN WO200155318-A2.  
XX PD 02-AUG-2001.  
XX PF 17-JAN-2001; 2001WO-US01332.  
XX PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209457.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225256.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
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### REFERENCE

AUTHORS Shibata, N

Kanno, H., Akiyama, J., Nishi, K., Katsuna, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Matsumura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Wakumoto, H., Sakauchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Izawa, M., Ohara, E., Watahiki, K., Itoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system—384 format sequencing pipeline with 384 multipipillary sequencer Genome Res. 10 (11), 1757–1771 (2000).

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VERSION
BC024803.1 GI:19354130
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ORGANISM
Mus musculus
REFERENCE
1 (bases 1 to 1877)
AUTHORS
Strausberg, R.
TITLE
Direct Submission
JOURNAL
Submitted (01-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK
NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT
Contact: MGC help desk
Email: gcgaps-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: ang@bcm.tmc.edu
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Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6671659
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REFERENCE			
1 (bases 1 to 1201)			
AUTHORS			
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.			
TITLE			
Full-length cDNA libraries and normalization			
JOURNAL			
Unpublished			
COMMENT			
Genoscope - Centre National de Sequencage			
BP 191 91006 EVRY cedex - France			
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr			
Library was constructed by Life Technologies, a division of			
Invitrogen. This sequence belongs to sequence cluster 3877.r For			
more information about this cluster, see			
http://www.genoscope.cns.fr/			
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Feng Liang Email : fliang@lifetech.com URL :			



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VERSION BX445032.1 GI:30778289
KEYWORDS EST.
SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3877.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS1AF006ZHL10P1&cluster=3877.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS1AF006ZHL10P1.
FEATURES
Location/Qualifiers
1..1201
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enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
BASE COUNT 281 a 325 c 326 g 221 t 48 others
ORIGIN
Query Match 41.5%; Score 921; DB 13; Length 1201;
Best Local Similarity 98.4%; Pred. No. 5.8e-207;
Matches 946; Conservative 4; Mismatches 9; Indels 2; Gaps 2;
QY 243 GAGCCCTCGCGCGCGCATGGCCACAGGCTGACCTGACCCGCTTCACCGACAGTA 302
Db
60 GATCCCTCGCGCGCGCATGGCCACAGGCTGACCTGACCCGCTTCACCGACAGTA 119
QY 303 CCAGCTCTAGAGGATATTGGCAAGGGGGCTTTCTGTGTGTCGAGCGCTGTGCAAGT 362
Db
120 CCAGCTCTAGAGGATATTGGCAAGGGGGCTTTCTGTGTGTCGAGCGCTGTGCAAGT 179
QY 363 CTGCACCGGCATGAGTATGCAGCCCAAGATCATCAACCAAGAGCTGTGCAGCAGAGA 422
Db
180 CTGCACCGGCATGAGTATGCAGCCCAAGATCATCAACCAAGAGCTGTGCAGCAGAGA 239
QY 423 TCACCAGAGCTGGAGAGAGGCTCGGATCTGCGCGCTTCTGAAGCATTCACACATCGT 482
Db
240 TCACCAGAGCTGGAGAGAGGCTCGGATCTGCGCGCTTCTGAAGCATTCACACATCGT 299
QY 483 GCGTCTCCACGACAGCATCTCCGAGGAGGCTTCCACTACCTGGTCTGATCTGGTGC 542
Db
300 GCGTCTCCACGACAGCATCTCCGAGGAGGCTTCCACTACCTGGTCTGATCTGGTGC 359
QY 543 TGGTGGGAGCTCTTTGAAGACATTTGGCGAGAGAGTACTACAGCGAGGCTGATGCCAG 602
Db
360 TGGTGGGAGCTCTTTGAAGACATTTGGCGAGAGAGTACTACAGCGAGGCTGATGCCAG 419
QY 603 TCACCTGTATCCAGACATCTGGAGGCGCTTCTCCATTGTCAACAAATGGGGTCTGCCA 662
Db
420 TCACCTGTATCCAGACATCTGGAGGCGCTTCTCCATTGTCAACAAATGGGGTCTGCCA 479
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Db
480 CAGAGACTTCAAGCCGGAGACCTGCTCTGCGCACAGATGTCAGAGGGGCTGCAGTGA 539
QY 723 GCTGGCAGACTTCGGCGCTAGCTATCGAGGTGCAGGGGGACCGAGGCTATGTTGGTTT 782

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	Query Match	39.6%;	Score 877.6;	DB 9;	Length 954;
	Best Local Similarity	99.9%;	Pred. No. 1e-196;		
	Matches 877;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0
QY	231	CGAGGCGACGCCGAGCCGCTCCGCGCGCCGCAATGCCACACACGGGTGACCTGCACCCCGCTT	290		
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QY	291	CACCGACAGTACACAGCTCTACAGAGATATTGGCAAGGGGGCTTTCTCTGTGTCCCAAGC	350		
DB	137	CACCGACAGTACACAGCTCTACAGAGATATTGGCAAGGGGGCTTTCTCTGTGTCCCAAGC	196		
QY	351	CTGTGTCAAGCTCTGCAACGGCCGATGAGTATGTCAGCGCAAGATCATCAACACCAAGAAGCT	410		

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411 GTCAGCCAGATCACCAGAAAGCTGGAGAGAGAGCTGGATCTGCCGCTTCTGAAGCA 470
Db
257 GTCAGCCAGATCACCAGAAAGCTGGAGAGAGAGCTGGATCTGCCGCTTCTGAAGCA 316
QY
471 TTCACACATCGTGTCTCCACACAGCATCTCCGAGAGGGCTTCCACTACTCGTCTT 530
Db
317 TTCCACATCGTGTCTCCACACAGCATCTCCGAGAGGGCTTCCACTACTCGTCTT 376
QY
531 CGATCTGTGTCATCTGTGGGAGCTCTTTGAAGACATCTGTGGGAGAGAGTACTACAGCA 590
Db
377 CGATCTGTGTCATCTGTGGGAGCTCTTTGAAGACATCTGTGGGAGAGAGTACTAMAGCA 436
QY
591 GGTGATGTCAGTCACTGTATCCACAGCATCTGTGGAGCGCTTCTCCATGTTCACCAAT 650
Db
437 GGTGATGTCAGTCACTGTATCCACAGCATCTGTGGAGCGCTTCTCCATGTTCACCAAT 496
QY
651 GGGGTCTGTCCACAGACCTCAAGCCGAGAACTGTCTTGTGGCAGCAAGTGCAGAGG 710
Db
497 GGGGTCTGTCCACAGACCTCAAGCCGAGAACTGTCTTGTGGCAGCAAGTGCAGAGG 556
QY
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Db
557 GGTGATGTCAGTCACTGTATCCACAGCATCTGTGGAGCGCTTCTCCATGTTCACCAAT 616
QY
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Db
677 GTATGCCAAGCTGTGGACATCTGGGAGTGTGGGATGTGATCTCTTCTCTCTCTCTCT 736
QY
891 CTACCCACCTCTGTGGAGGAGCAGCAGCAGCTGTACCCAGTCTGTACAGATCAGGCTGTGC 950
Db
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QY
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797 CTATGACTTCCGCTCCCTGAGTGGGACACCGTCACTCTTGAAGCAAAACCTCATCAA 856
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1011 CCGAGTCTGACATCAACCTTCCAGAGCGATCAGCCCAAGAGGCTTGAAGCACC 1070
Db
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917 GTGGGTCTGCCAACGCTCCAGGTAGCATCCATGATGC 954

RESULT 10
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LOCUS
DEFINITION
AGENCOURT_14367396 NIH_MGC_181 Homo sapiens cdna clone
IMAGE:30397472 5', mRNA sequence.
ACCESSION
CD515849
VERSION
CD515849.1 GI:31447567
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 866)
NIH-MGC http://mgc.nci.nih.gov/.
REFERENCE
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
AUTHORS
Unpublished
TITLE
Office of Cancer Genomics
JOURNAL
Contact: Daniela S. Gerhard, Ph.D.
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: c9apbs-r@mail.nih.gov

```

Tissue Procurement: Dr. Michael Brownstein  
 cDNA Library Preparation: Invitrogen Corp  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: NDAM480 row: n column: 09  
 High quality sequence stop: 694.

FEATURES  
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 Db 1 TGGCCACACCGGTGACCTCCACCCCGCTTCACCGACAGTACCAGCTCTACGAGATATTG 60  
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 Db 61 GCAAGGGGGCTTCTCTGTGTCCGACGCTGTGTCAAGCTCTGCACCGCCACGACTATG 120  
 QY 383 CAGCCAGATCATCAACACCAAGAGCTGTCTAGCCAGAGATCACCAGAGAGTGGAGAGAG 442  
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 QY 443 AGGCTCGATCTCGCGCTTCTGAAAGCATTCACACATCTGCTTCCACAGACATCT 502  
 Db 181 AGGCTCGATCTCGCGCTTCTGAAAGCATTCACACATCTGCTTCCACAGACATCT 240  
 QY 503 CCGAGAGGGCTTCCACTACTCTGTGTCTTCCGATCTGTGTCACTGTGGGAGCTCTTTCAAG 562  
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RESULT 11

AK078311

LOCUS

DEFINITION

AK078311 3613 bp mRNA linear HTC 05-DEC-2002

Mus musculus adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:6430591H15

product:CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II ISOFORM GAMMA-C PROTEIN KINASE II homolog [Sus scrofa], full insert sequence.

ACCESSION AK078311

VERSION AK078311.1 GI:26347132

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE

1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Carninci, P. and Hayashizaki, Y.

AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE

2

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE

3

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kusunagi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, F., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, K., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE

4

AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamada, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okado, F., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,

Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyo-oka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohtsuki, S. and Hayashizaki, Y.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

MEDLINE 21085660

PUBMED 11217851

REFERENCE

5

AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

MEDLINE 12187851

REFERENCE

6 (bases 1 to 3613)

AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, I., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscl.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

MEDLINE

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://phantom.gsc.riken.go.jp/

FEATURES

source

1. 3613

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68. 1153

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/protein\_id="BAC37215.1"

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3599. 3604

polyA\_signal

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QY	1268	GGCTGTGTGGAACAAGCCCAAGAGTTTATCTCAACAAGAAAGCAGATGGAGTCAAGCCCCAGA	1377
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QY	1328	CGAATAGCACCAAAACAGTGCACGCCCAACACAGCCCCAAAGAGGACGCTTCCTCTCTGGG	1387
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QY	1388	CCCTGGAGCCTCAACACCAACCGCTTCATCAATAACCAAGTCAGCGGATTAAGAGAGTCTTCTG	1447
Db	1201	CAGAGACGAGNATCTCAAGCTGAGAAACAAGAAATCATTAAGATCACAGAACACTGA	1266
QY	1448	ACAGTGGCAATACCAACCATAGAGGATGAAGAGCTAAAGCCCCGGAAGAGAGATCATTA	1507
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QY	1508	AGACCCGGAGGAGCTCATCGAGCGCGTCAACAAGCGGTGACTTTGAGGCGCTACGCAATCT	1567
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QY	1568	ACTTCGAGAAACCTTGCTGGCCCAAGAACAGCAGCCGATCCACACGACCATCTTGAACCCAC	1627
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QY	1688	TTGACGGGCAAGGCGCGCCCGCCAGCAGCTCTGAGGAGACCGCGGTGTGGCAGCCGCC	1747
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QY	1748	CGAGCGCAGTGGCAAGACGTGCATCTCCACTGCTCGGGGCGCGCTGTGGCCCGCGCTGC	1807
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QY	1808	AGTGAAGCCA	1817
Db	1621	AGTGAGCTCA	1630
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VERSION	BI553655.1	GI:15440967	
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SOURCE			
ORGANISM			
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			Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE			
AUTHORS			NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE			National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL			Unpublished
COMMENT			Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:ncgbs-f@mail.nih.gov">ncgbs-f@mail.nih.gov</a> Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.

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QY	295	GACGAGTACCAGCTCT	ACGAGGATATGCGACAGGGGGCTTCTCTGTCGTCGACGCGTGT	354
Db	123	GACGAGTACCAGCTCT	ACGAGGATATATGGCAAGGGGGCTTCTCTGTGGTCCGACGCGTGT	182
QY	355	GTCAGGCTCTGCACGG	CCCATGAGTATGCGACCAAGATCATCAACACCAAGAGCGTGCA	414
Db	183	GTCAGGCTCTGCACGG	CCCATGAGTATGCGACCAAGATCATCAACACCAAGAGCGTGCA	242
QY	415	GCCAGAGATCACAGA	AGCTGGAGAGAGGCTTCGAGTCTGCCGCTTCTTGAGGATTC	474
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 QY 901 TTTAACC 907

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 DEFINITION mRNA sequence.  
 ACCESSION BI597219  
 VERSION BI597219.1 GI:15490158  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 764)  
 NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: gcrabs@remail.nih.gov  
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
 Toshiyuki and Piero Carninci (RIKEN)  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: L1A11766 row: m column: 22  
 High quality sequence stop: 756.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5302845"  
 /tissue\_type="hypothalamus"  
 /lab\_host="DH10B"  
 /clone\_lib="NTH\_MGC\_96"  
 /notes="Organ: brain; Vector: pBluescriptR (modified  
 pBluescript KS+); Site.1: BamHI; Site.2: SalI-XhoI (gtcgag  
 ); Oligo-dT primed using primer 5'-TTTTTTTTTTTNN-3',  
 size-selected for average insert size 2.3 kb and  
 normalized to ROT 5. This is a primary library enriched  
 for full-length clones and constructed using the  
 Cap-trapper method (Carninci, in preparation). Library

FEATURES  
 source

constructed by M. Brownstein (NHGRI/NHGRI, National  
 Institutes of Health). Note: this is a NIH\_MGC Library."  
 BASE COUNT 160 a 230 c 225 g 149 t  
 ORIGIN  
 Query Match 34.1%; Score 756.4; DB 12; Length 764;  
 Best Local Similarity 99.9%; Pred No. 4.4e-168;  
 Matches 757; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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 QY 6 GAGCGACGCGAGCCCGTCCCGCCCATGGCCACCAAGGTGACCTGACCCGCTTC 65  
 Db |||||  
 QY 292 ACCGAGAGTACAGCTCTACAGAGATATTGGCAAGGGGCTTCTCTGTGGTCCGACGC 351  
 Db |||||  
 QY 66 ACCGAGAGTACAGCTCTACAGAGATATTGGCAAGGGGCTTCTCTGTGGTCCGACGC 125  
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 QY 126 TGTGTAAAGTCTGCAACCGCCCATGATGATGACGCAAGATCATCAACCAAGAACTG 185  
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 QY 412 TCAGCCACAGATCACAGAGCTGGAGAGAGAGCTCGGATCTGCCGCTTCTGAAGCAT 471  
 Db |||||  
 QY 186 TCAGCCACAGATCACAGAGCTGGAGAGAGCTCGGATCTGCCGCTTCTGAAGCAT 245  
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 QY 472 TCCAAATCTGTGGTCTCCACAGACATCTCCGAGAGGGCTTCCACTTACTGCTTTC 531  
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 QY 246 TCCAAATCTGTGGTCTCCACAGACATCTCCGAGAGGGCTTCCACTTACTGCTTTC 305  
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 QY 532 GATCTGTGCTACTGTGGGAGCTCTTGAAGACATTTGGCGAGAGTACTACAGGAG 591  
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 QY 306 GATCTGTGCTACTGTGGGAGCTCTTGAAGACATTTGGCGAGAGTACTACAGGAG 365  
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 QY 592 GGTGTGCGAGTCACTGTATCCAGAGATCTCGAGAGCGCTTCTCCATGTACCCAAATG 651  
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 QY 712 GGTGAGTGAAGCTGGGAGACTTGGGCTAGCTATCAGGTGAGGGGACCCAGCAGCA 771  
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 QY 486 GGTGAGTGAAGCTGGGAGACTTGGGCTAGCTATCAGGTGAGGGGACCCAGCAGCA 545  
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 QY 772 TGGTTGGTTTCTGTGGCACAACAGGCTACCTGTCCTGAGGTCTTCGCAAGAGGG 831  
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 QY 546 TGGTTGGTTTCTGTGGCACAACAGGCTACCTGTCCTGAGGTCTTCGCAAGAGGG 605  
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 QY 606 TATGCAAGCCCTGTGGGAGACTTGGGCTAGTGGGCTGATCTGTACATCTGCTGTGGGC 665  
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 QY 892 TACCCACCCCTTCTGGGAGCAGGACCAAGCTGTACCAAGATCAAGGCTGTGGTGC 951  
 Db |||||  
 QY 666 TACCCACCCCTTCTGGGAGCAGGACCAAGCTGTACCAAGATCAAGGCTGTGGTGC 725  
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 QY 952 TATGACTTCCCGTCCCTGAGTGGGACACCGTCACTCC 989  
 Db |||||  
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Search completed: October 10, 2003, 07:48:15  
 Job time : 4899 secs

Result No.	Score	Query		Length	DB	ID	Description
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2	214	9.6	1480	4	US-09-016-434-1454	Sequence 1454, Ap	
3	185.8	8.4	1282	2	US-08-878-989-12	Sequence 12, Appl	
4	185.8	8.4	1282	3	US-09-272-736-12	Sequence 12, Appl	
5	185.8	8.4	1282	4	US-09-016-434-953	Sequence 953, App	
6	185.2	8.3	1349	1	US-07-951-715A-20	Sequence 20, Appl	
7	185.2	8.3	1349	2	US-08-459-448A-20	Sequence 20, Appl	
8	185.2	8.3	1349	3	US-08-453-595A-20	Sequence 20, Appl	
9	185.2	8.3	1349	3	US-08-459-504B-20	Sequence 20, Appl	
10	185.2	8.3	1349	3	US-08-459-444-20	Sequence 0, Appli	
11	185.2	8.3	1349	4	US-09-547-422-20	Sequence 0, Appli	
12	183.8	8.3	3471	2	US-08-715-568A-2	Sequence 2, Appli	
13	181.4	8.2	423	4	US-09-016-434-1098	Sequence 1098, Ap	
14	174	7.8	62804	4	US-09-800-960-3	Sequence 3, Appli	
15	173.2	7.8	1694	4	US-09-579-664B-3	Sequence 3, Appli	
16	171.2	7.7	1733	4	US-09-620-312D-526	Sequence 526, App	
17	163	7.3	2132	2	US-09-159-385-3	Sequence 3, Appli	
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19	153	6.9	2165	4	US-09-620-312D-809	Sequence 809, App	
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Db 426 GAGAGTACTACAGTGAAGCAGATGCGCAGCCTGTATACATCAAGATTCCTGGAGAGTGA 485  
QY 635 TCCATTGTCACCAATGSGGCTGCTCCAGAGACCTTCAAGCCGGAGAACCTCTCTCGG 694  
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## RESULT 2

US-09-016-434-1454  
; Sequence 1454, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Sellhammer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,434  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0002 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1454:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1480 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: 9790789  
US-09-016-434-1454

Query Match 9.6%; Score 214; DB 4; Length 1480;  
Best Local Similarity 54.8%; Pred. No. 3e-38;  
Matches 490; Conservative 0; Mismatches 395; Indels 9; Gaps 3;

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QY 888 GSGCTACCCACCTCTGGGAGGACCCAGACAGCTGTACAGGATCAAGGCTGTG 947  
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QY 1008 CAACGATGCTGACCATCAACCTCCAGAGCATCAAGCCCATGAGGCGCTTGA 1067  
DB 906 CCGGCACTTGTGAGAGAGACCCAGAGAAAGATTCACTGTGAGGAGGCTTGA 965  
QY 1068 CCGGTGGGTCTGCAACGCTCCAGGTAGCATCCATGATGCAACAGAGAGACTGTGA 1127  
DB 966 CCCATGATTCAGGAGATACAGCTCTAGATAAGATATCCACAGTCTGATGATGA 1025  
QY 1128 GTGCTGAAAAGTTCAATGCCAGGAAAGCTCAAGGAGGACCATCTTCAACCA 1181  
DB 1026 G---ATCAAGAAAGCTTTGCCAAGAGCAAGTGAAGGAGGCTTCAATGCCAC 1076

RESULT 3

US-08-878-989-12  
; Sequence 12, Application US/08878989  
; Patent No. 5885803  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Hillman, Jennifer L.

APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl G.  
APPLICANT: Lal, Preeti  
APPLICANT: Goli, Surya K.  
APPLICANT: Shah, Purvi  
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/878,989  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0321 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: PROSNOT06  
CLONE: 827431  
US-08-878-989-12

Query Match 8.4%; Score 185.8; DB 2; Length 1282;  
Best Local Similarity 52.8%; Pred. No. 4.8e-32;  
Matches 475; Conservative 0; Mismatches 413; Indels 12; Gaps 3;

QY 288 CTTCCAGGAGTACAGCTCTACGAGGATATTTGGCAAGGGCTTCTCTGTGTCGG 347  
DB 230 CATCAGCAGCTCTACGAGATCCGAGAGGCTCGGCTCGGGTGCCTTCTCCGAGTGT 289  
QY 348 ACCTGTGTCAAGCTCTGACCGGCCATGAGTATCGAGCCAGAGATCATCAACCAAGAA 407  
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DB 350 CTTCCGGGCAAGGAGGCC---TGGTGGAGAACAGATCGCAGTCTCGTAGGATCAG 406  
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DB 467 CATGGAATGCTGACGGGTGGAGCTGTTGACCGCATCATGGAGCGGGCTTCTACAC 526  
QY 588 CGAGGCTGATGCTACTGATCTCCAGAGATCTGAGGCGCTTCTCCATTGTGACCA 647  
DB 527 AGAAGAGGATGCCACCATCTGGTGGGTGAGTCTTGGCCGCTCTCTCTACCTGCACAG 586





QY 1068 CCGTGGTCTGCCAGCTCCACGCTAGCTCCATGATGACACAGCAGGAGACTGTGA 1127  
 DB 1001 CCITTTGATCTTTGGGACACAGCGCTTGGCAGGACACATCTAGGTTTGTAGTGAGCA 1060  
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 DB 1061 GATCCGGAAGAACTT---TGCTTGGACACACTGGAAGCGAGCCCTCAATGCCACCTTGT 1117

RESULT 5  
 US-09-016-434-953  
 ; Sequence 953, Application US/09016434  
 ; Patent No. 6500938  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Janice Au-Young  
 ; APPLICANT: Jeffrey J. Seilhamer  
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
 ; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
 ; NUMBER OF SEQUENCES: 1490  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 ; STREET: 3174 PORTER DRIVE  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/016,434  
 ; FILING DATE: HEREWITH  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Zeller, Karen J.  
 ; REGISTRATION NUMBER: 37,071  
 ; REFERENCE/DOCKET NUMBER: PA-0002 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (650) 855-0555  
 ; TELEFAX: (650) 845-4166  
 ; INFORMATION FOR SEQ ID NO: 953:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1282 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: PROSNOT06  
 ; CLONE: 827431  
 ; US-09-016-434-953

Query Match 8.4%; Score 185.8; DB 4; Length 1282;  
 Best Local Similarity 52.8%; Pred. No. 4.8e-32;  
 Matches 475; Conservative 0; Mismatches 413; Indels 12; Gaps 3;

QY 288 CTTACCCAGGAGTACCAGCTCTACGAGGATATTGGCAAGGGGGCTTCTCTGTTGGTCCG 347  
 DB 230 CATCAGCAGCTCTACGAGATCCGCGAGAGGCTCGGCTCGGTTGCTCTCCGAGGTTGT 289  
 QY 348 AGCTGTCTCAAGCTCTGACCGGCCATGATATGACGACGACATCATCACACAGAA 407  
 DB 290 GTGTGCCCGCAGGAGGGGGCTCCGACACCTCGTGGCCCTCAAGTGCATCCGCCAAGAGGC 349  
 QY 408 GCTGTCTACCGAGATCACAGAGCTGAGAGAGGCTCGGATCTGCCCTTCTGAA 467  
 DB 350 CTTCCGGGGCAGGAGGCC---TGGTGGAGACAGATGCGAGTGTCTCCGTAGGATCAG 406

QY 468 GCATTCACACATCGTGGTCTCCACACAGACATCTCCGAGGAGGGCTTCCACTACCTGGT 527  
 DB 407 TCACCCACACATCGTGGTCTCCGAGGATGTCCACGAGAGCCCTTCCACCTCTACTGGC 466  
 QY 528 CTTGATCTGTCTACTGTTGGGAGCTCTTTGAGACATATTGTGGCGAGAGACTACTACAG 587  
 DB 467 CATGGAATGTGTGAGGGTGGGAGCTTTTGGACCGCATCATGAGCGGGGTCTCTACAC 526  
 QY 588 CGAGGCTGATGCCAGTCACTGTATCCAGCATCTCGGAGCGGCTTCTCCATTTGTCACA 647  
 DB 527 AGAAGAGATGCCAGCCATCTGGTGGTCAAGTCTTGGCGCGCTCTCTACTCCACAG 586  
 QY 648 AATGGGGTCTCCACAGAGACCTCAAGCCGAGAACTCTGTTCTTGGCAGCAAGTCAAA 707  
 DB 587 CTTGGGATCTGACCGGGACCTCAAGCCGAAACCTCTGTATGTCACCGCCCTTGA 646  
 QY 708 AGGGGTGCAAGTGTGAGCTGCGCTAGCTATCGAGTTCAGGAGGAGGAGGAGGAGCA 767  
 DB 647 GGACTCGAAGATCATGTTGCTCTGACTTTGGACTCTCCAAATCCAGCTGGGAAATGCT 706  
 QY 768 GCATGTTTGGTCTGCTGGCACACAGGCTACCTGTCCCTGAGTCTTTCGCAAGA 827  
 DB 707 AGGACCGGCTG-----TGGACCCCTGGATATGTGGCCACAGAGCTCTTGGAGCAAA 760  
 QY 828 GCGTATGCAAGCTGTGGACATCTGGCATGTGGGTGATCTGTACATCTCTCTGCT 887  
 DB 761 ACCCTACGGGAAGCGCTAGATGTGGGCTCTGAGGCTCTATCTCTACTCTCTCTGTG 820  
 QY 888 GGGCTACCCACCTCTTGGGACGAGGACGACAGCTGTACACAGCATCAAGCTGG 947  
 DB 821 TGGGTACCCCTCTTACGACGAGAGGAGCCCTGAGCTCTTACGACGATCTCTGAGGC 880  
 QY 948 TGCTATGACTTCCCGTCCCTGAGTGGGACACCTCTCTCTGAGGCAAAACCTCAT 1007  
 DB 881 CAGCTATGAGTTGACTNTCTTCTGGATGACATCTCAAGATCAGGAGGAGGAGCTTAT 940  
 QY 1008 CAACGAGATGTCACCATCAACCTGCAAGCGCATCACAGCCATGAGGAGGAGGAGCA 1067  
 DB 941 TCGGACCTTCTGGAGCGAGACCTTCAGAGAGGTTTCACTGCGACAGGCTTGGGGA 1000  
 QY 1068 CCGTGGTCTCCCAAGCTTCCAGGCTAGCTATCCATGATGACAGACAGGAGACTGTGGA 1127  
 DB 1001 CTTTGGATCTTTGGGACACAGGCTTGGCAGGAGCATCTTAGGTTTGTGAGTGAGCA 1060  
 QY 1128 GTGTCTGAAGAAAGTTCAATGCCAGGAGAAAGCTCAAGGAGGAGGAGGAGGAGGAG 1187  
 DB 1061 GATCCGGAAGAACTT---TGGTGGACACACTGGAAGGAGGAGGAGGAGGAGGAGGAG 1117

RESULT 6  
 US-07-951-715A-20  
 ; Sequence 20, Application US/07951715A  
 ; Patent No. 5625136  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Koziel, Michael G.  
 ; APPLICANT: Desai, Nalini M.  
 ; APPLICANT: Lewis, Kelly S.  
 ; APPLICANT: Kramer, Vance C.  
 ; APPLICANT: Warren, Gregory W.  
 ; APPLICANT: Evola, Stephen V.  
 ; APPLICANT: Crossland, Lydie D.  
 ; APPLICANT: Wright, Martha S.  
 ; APPLICANT: Merlin, Ellis J.  
 ; APPLICANT: Launis, Karen L.  
 ; APPLICANT: Rothstein, Steven J.  
 ; APPLICANT: Bowman, Cindy G.  
 ; APPLICANT: Dawson, John L.  
 ; APPLICANT: Dunder, Erik M.  
 ; APPLICANT: Pace, Gary M.  
 ; APPLICANT: Suttie, Janet L.  
 ; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
 ; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE





;  
;     APPLICANT: Crossland, Lyle D.  
;  
;     APPLICANT: Wright, Martha S.  
;  
;     APPLICANT: Merlin, Ellis J.  
;  
;     APPLICANT: Launis, Karen L.  
;

APPLICANT: Bowman, Cindy G.  
 APPLICANT: Dawson, John L.  
 APPLICANT: Dunder, Erik M.  
 APPLICANT: Pace, Gary M.  
 APPLICANT: Suttie, Janet L.  
 TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
 TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
 NUMBER OF SEQUENCES: 94  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: No. 6075185artis Corporation  
 STREET: 3054 Cornwallis Road  
 CITY: Research Triangle Park  
 STATE: NC  
 COUNTRY: USA  
 ZIP: 27709  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/459,504B  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/459,595  
 FILING DATE: 02-JUN-1995  
 APPLICATION NUMBER: US 07/951,715  
 FILING DATE: 25-SEP-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/772,027  
 FILING DATE: 04-OCT-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meigs, J. Timothy  
 REGISTRATION NUMBER: 38,241  
 REFERENCE/DOCKET NUMBER: GC1577/CIP/DIV  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (919)541-8587  
 TELEFAX: (919)541-8689  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1349 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 3..1226  
 OTHER INFORMATION: /note= "cDNA sequence for maize  
 OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as  
 OTHER INFORMATION: disclosed in Figure 30."  
 JS-08-459-504B-20

	5267	5268	5269	5270	5271	5272	5273	5274	5275	5276	5277	5278	5279	5280	5281	5282	5283	5284	5285	5286	5287	5288	5289	5290	5291	5292	5293	5294	5295	5296	5297	5298	5299	5300	5301	5302	5303	5304	5305	5306	5307	5308	5309	5310	5311	5312	5313	5314	5315	5316	5317	5318	5319	5320	5321	5322	5323	5324	5325	5326	5327	5328	5329	5330	5331	5332	5333	5334	5335	5336	5337	5338	5339	5340	5341	5342	5343	5344	5345	5346	5347	5348	5349	5350	5351	5352	5353	5354	5355	5356	5357	5358	5359	5360	5361	5362	5363	5364	5365	5366	5367	5368	5369	5370	5371	5372	5373	5374	5375	5376	5377	5378	5379	5380	5381	5382	5383	5384	5385	5386	5387	5388	5389	5390	5391	5392	5393	5394	5395	5396	5397	5398	5399	5400	5401	5402	5403	5404	5405	5406	5407	5408	5409	5410	5411	5412	5413	5414	5415	5416	5417	5418	5419	5420	5421	5422	5423	5424	5425	5426	5427	5428	5429	5430	5431	5432	5433	5434	5435	5436	5437	5438	5439	5440	5441	5442	5443	5444	5445	5446	5447	5448	5449	5450	5451	5452	5453	5454	5455	5456	5457	5458	5459	5460	5461	5462	5463	5464	5465	5466	5467	5468	5469	5470	5471	5472	5473	5474	5475	5476	5477	5478	5479	5480	5481	5482	5483	5484	5485	5486	5487	5488	5489	5490	5491	5492	5493	5494	5495	5496	5497	5498	5499	5500	5501	5502	5503	5504	5505	5506	5507	5508	5509	5510	5511	5512	5513	5514	5515	5516	5517	5518	5519	5520	5521	5522	5523	5524	5525	5526	5527	5528	5529	5530	5531	5532	5533	5534	5535	5536	5537	5538	5539	5540	5541	5542	5543	5544	5545	5546	5547	5548	5549	5550	5551	5552	5553	5554	5555	5556	5557	5558	5559	5560	5561	5562	5563	5564	5565	5566	5567	5568	5569	5570	5571	5572	5573	5574	5575	5576	5577	5578	5579	5580	5581	5582	5583	5584	5585	5586	5587	5588	5589	5590	5591	5592	5593	5594	5595	5596	5597	5598	5599	5600	5601	5602	5603	5604	5605	5606	5607	5608	5609	5610	5611	5612	5613	5614	5615	5616	5617	5618	5619	5620	5621	5622	5623	5624	5625	5626	5627	5628	5629	5630	5631	5632	5633	5634	5635	5636	5637	5638	5639	5640	5641	5642	5643	5644	5645	5646	5647	5648	5649	5650	5651	5652	5653	5654	5655	5656	5657	5658	5659	5660	5661	5662	5663	5664	5665	5666	5667	5668	5669	5670	5671	5672	5673	5674	5675	5676	5677	5678	5679	5680	5681	5682	5683	5684	5685	5686	5687	5688	5689	5690	5691	5692	5693	5694	5695	5696	5697	5698	5699	5700	5701	5702	5703	5704	5705	5706	5707	5708	5709	5710	5711	5712	5713	5714	5715	5716	5717	5718	5719	5
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Db 129 GCCGGGCGCAGTACACGAGCGCGCGCGGAGCTCTCGCGGCATCTGTCAGATC 188  
QY 631 GTTCTCATATGTCACCAAAATGGGGTGTCTCCACAGAGACCTCAAGCGGAGAACCTGCTT 690  
Db 189 GTGCACACCTGCTCCATCCATGGGGTGTATGACCGGGGATCAAGCCGAGAACTTCCTG 248  
QY 691 CTGCCAGCAAGTGAAGGGGCTGCAGTGAAGCTGGAGACTTGGCCTAGCTATCAG 750  
Db 249 CTGCTACAGAGAGAGAGAGCGCCCTCAAGGCCACCGACTTGGCCCTCGCTTC 308  
QY 751 GTGCAGGGGACAGCAGCATGTTGTTGTTGCTGGCACACAGGCTACCTGTCCT 810  
Db 309 TTCAAGAGGGGAGCTGCTCAGG---GACATGTCGGCAGCGCTACTACATCGCGCC 365  
QY 811 GAGTCTCTTGGCAAGAGCGCTATGCGAAGCCTGTGGACATCTGGGCATGTGGGTGATC 870  
Db 366 GAGGTGCT---CAAGAGAAATGAGCGCCCGGAGCGGACATCTGGAGCGTCGCTCATG 422  
QY 871 CTGTACATCTGCTGCTGGGCTACCCACCTCTCTGGGAGGAGCACCAAGCTGTAC 930  
Db 423 CTCTACATCTTCTCGCGGGTGTCTTCCCTTCTGGGAGAGAGAGAGAGAGAGAGATCTTC 482  
QY 931 CAGCAGATCAAGCTGTGGTGTCTTCCCTTCTGGGAGAGAGAGAGAGAGAGAGATCTTC 990  
Db 483 ACCGCCATCTGCGAGGGGAGCTGACCTCTCCAGCGAGCCATGSCCAGACATCTCGCG 542  
QY 991 GAAGCCAAACATCATCAACAGCATGCTGACCATCAACCTGCGCAGCGGATCACAGCC 1050  
Db 543 GGAGCCAAAGATCTGTCAAGAGATGCTCAACATCAACCCCAAGAGAGCGCTCACGGG 602  
QY 1051 CATGAGCCCTGAAGCAGCCCTGGTGTCTGCAAGCTCCAGCTGATCATCATGATGAC 1110  
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QY 1111 AGACAGAGAGCTGTGGATGTCTGAAAGATTCATGCGCAGAGAGAGAGAGAGAGAG 1170  
Db 663 GACAAGTGTGTTCTGAGAGGCTCAAGAGCTTCCAGGGGATGAACAGATTCAAGAAAGCA 722  
QY 1171 ATCTCCACCAACCAT 1184  
Db 723 GCATGAGGATCAT 736

RESULT 10

US-08-459-444-20  
; Sequence No, Application US/0845944A  
; Patent No. 6121014  
; GENERAL INFORMATION:

APPLICANT: Kozziel, Michael G.  
Desai, Nalini M.  
Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.  
Lauis, Karen L.

TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED  
NUCLEIC ACID CODING SEQUENCE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,444A  
FILING DATE: 02-Jun-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIF/DIV6  
TELEPHONE: (919)541-8587  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: /note= "cDNA sequence for maize  
pollen-specific calcium dependent protein kinase gene  
disclosed in Figure 30."  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1349 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
NAME/KEY: CDS  
LOCATION: 3..1226  
SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-08-459-444-20

Query Match 8.3%; Score 185.2; DB 3; Length 1349;  
Best Local Similarity 55.2%; Pred. No. 6.6e-32;

Matches 405; Conservative 0; Mismatches 323; Indels 6; Gaps 2;

QY 451 ATCTCGCGCTTCTGAAGCATTCACATCGCTCTCCACAGACACATCTCCGAGGAG 510  
Db 9 ATGCACACCTCTCGCGCCACCCCAAGCTGTGTGGGCTCCGCGCGCTACGAGGACAG 68  
QY 511 GGCTTCCACTACTTGGTCTTTCGATCTGTGCTACTGTGTGGGAGCTCTTTGAAGACATFTG 570  
Db 69 CAGAGCGTGCACCTCGTCTATGGAGCTGTGCGGGGGGGAGCTCTTCGACCGCATC 128  
QY 571 GCGAGAGAGTACTACAGCGAGCTGATGCGAGTCACTGTATCCAGAGATCTTGGAGGCC 630  
Db 129 GCCGGGGCCAGTACACGAGCGCGCGCGCGGAGCTGTGCGCGCCATCTGTCAGATC 188  
QY 631 GTTCTCCATTGTCAACAAATGGGGTGTCTCCACAGAGACCTCAAGCGGAGAACCTGCTT 690  
Db 189 GTGCACACCTGCTCCATCCATGGGGTGTATGACCGGGACATCAAGCCGAGAACTTCCTG 248  
QY 691 CTGCCAGCAAGTGAAGGGGCTGCAAGTGAAGCTTGGCAGACTTCGCCCTAGCTATCAG 750  
Db 249 CTGCTACGACAGGAGGAGCGCGCGCTCAAGGCCACCGGACTTCGCCCTCTCGCTTC 308  
QY 751 GTCCAGGGGACACAGCAGCATGTTGTTGCTGTGTCACACAGGCTACTGTCCTCT 810  
Db 309 TTCAAGAGGGGAGCTGCTCAGG---GACATGTCGGCAGCGCTACTACATCGGGGCC 365  
QY 811 GAGTCTCTTCCGAAAGAGCGCTATGGCAAGCCTGTGGACATCTGGGCTGTGGGTGATC 870  
Db 366 GAGGTGCT---CAGAGAGAAATGAGCGCCCGGAGCGGAGATCTGAGCGCTGCGCTCATG 422  
QY 871 CTGTACATCTGCTGTGGGCTACCCACCTCTCTGGGAGAGAGAGAGAGAGAGATCTTAC 930  
Db 423 CTCTACATCTTCTCGCGGGGCTGCTTCCCTTCTGGGAGAGAGAGAGAGAGAGATCTTTC 482  
QY 931 CAGCAGATCAAGCTGTGGTGTCTTCCCTTCTGGGAGAGAGAGAGAGAGAGATCTTTC 990  
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Db 543 GGAGCGAGGATCTCGTCAAGAAGATGCTCAACATCAACCCCAAGAGCGGCTCACGGCG 602  
QY 1051 CATGAGCGCCCTGAAGACCCCGTGGGTGTCGCAAGGCTCCACGGTAGCATCCATGATGAC 1110  
Db 603 TTCAGGTCTCAATCAACCATGATGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 662  
QY 1111 AGACAGGAGATGTGGAGTCTGTAAGAGTCTGTAAGAGTCTGTAAGAGTCTGTAAGAG 1170  
Db 663 GACAAAGTGTCTGCAAGGCTCAAGCAGTTCAGGCGCATGAACAGTTCAGAAAGCA 722  
QY 1171 ATCCTCACACCAT 1184  
Db 723 GCATTGAGGATCAT 736

## RESULT 11

US-09-547-422-20  
; Sequence 0, Application US/09547422  
; Patent No. 6320100  
GENERAL INFORMATION:  
APPLICANT: Koziel, Michael G.  
Desai, Malini M.  
Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.  
Launis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
INSECTICIDAL ACTIVITY IN MAIZE

## NUMBER OF SEQUENCES: 94

## CORRESPONDENCE ADDRESSES:

ADDRESS: No. 6320100artis Agribusiness Biotechnology Research, Inc.  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/547,422  
FILING DATE: 11-Apr-2000  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/459,595  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991

## ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-18805H  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8587  
TELEFAX: (919)541-8689

## INFORMATION FOR SEQ ID NO: /note= "cDNA sequence for maize

pollen-specific calcium dependent protein kinase gene as  
disclosed in Figure 30."

## SEQUENCE CHARACTERISTICS:

LENGTH: 1349 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 3..1226  
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-09-547-422-20

Query Match 8.3%; Score 185.2; DB 4; Length 1349;

Best Local Similarity 55.2%; Pred. No. 6.6e-32;

Matches 405; Conservative 0; Mismatches 323; Indels 6; Gaps 2;

QY 451 ATCTGCCGCTTCTGAAGCATTTCAACATGTTCCACGATGTTCCACGACGAGCATTCGAGGAG 510  
Db 9 ATGACACCATCTCCGGCCGCCCAACCTGGTGGGCTCCGGGGCGGTAGGAGCAAG 68

QY 511 GCCTTCCATPACCTGCTTTCGATCTGTCACCTGCTGCTGGGGAGCTCTTTGAAGACATTTG 570  
Db 69 CAGAGCGTGCACCTCTGTCATGAGCTGTGCGGGGGGGAGCTCTTGCACCGCATCATC 128

QY 571 GCGAGAGTACTACAGCGAGCTGATGCCAGTCACTGTATCCAGCAGCATCTCGAGGCC 630  
Db 129 GCCCGGGCCAGTACACAGGAGCGCGCCCGGAGCTGCTGGCGCCATCTGTCAGATC 188

QY 631 GTTCTCCATTGTCAACCAATGGGGTCTGTCACAGAGACCTCAAGCCGGAGAACCTCTT 690  
Db 189 GTGCACACCTGCCACTCCCATGGGGTGTGATGACCGGGGACATCAAGCCGAGAACTCTTG 248

QY 691 CTGGCCAGCAAGTGCAGAGGGGCTGCAGTGNAGCTGGCAGACTTCGGCTAGTCTCGAG 750  
Db 249 CTGCTCAGAGGAGGAGGAGCGCGCTCAAGCCACCGACTTCGGCTCTCGGCTTC 308

QY 751 GTGAGAGGGAGACCAAGCATGTTGTTTGTGCTGGCCACACAGGCTACTCTCCCT 810  
Db 309 TTCAGAGGAGGCGAGCTGCTCAGG---GACATCTGGGAGCGGCTACTACATCGCGCC 365

QY 811 GAGGTCTTCCCAAGAGCGCTATGGCAAGCCTTGGACATCTGGGCATGTGGGTGATC 870  
Db 366 GAGGTGCT---CAAGAGGAAGTACGGCCCGGAGCGCGACATCTGGAGGTGCGGCTC 422

QY 871 CTGTACTCTCTGCTGGGCTACCCAGCTTCTGGGAGGAGGAGGAGGAGGAGGAGGAGG 930  
Db 423 CTGTACTCTCTGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 482

QY 931 CAGCAGATCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 990  
Db 483 ACCGCACTCTGCGAGGCGAGCTTGACCTCTCCAGCGAGCATGGCCACACATCTCGCG 542

QY 991 GAAGCCAAACCTCATCAACAGATGCTGACCATCAACCTGCCAAGCGCATCACAGCC 1050  
Db 543 GGAGCCAGGATCTCTGTCAGAGATGCTCAACATCAACCCCAAGGAGCGGCTCACGGG 602

QY 1051 CATGAGGCTTGAAGCACCCGCTGGGTCTGCCAAGCTTCCACGCTAGCATCATCATGAC 1110  
Db 603 TTCAGGTCCTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 662

QY 1111 AGACAGGAGACTGTGAGTGTCTGAAAAGTCTAAAGTCTAAAGTCTAAAGTCTAAAGT 1170  
Db 663 GACACAGTGTGCTGACAGGCTCAAGCAGTTCAGGCGCATGAACACAGTTCAGAAAGCA 722

QY 1171 ATCCTCACACCAT 1184  
Db 723 GCATTGAGGATCAT 736

## RESULT 12

US-08-715-568A-2  
; Sequence 2, Application US/08715568A  
; Patent No. 5856463

## GENERAL INFORMATION:

APPLICANT: Prydz, Hans Peter Blankenborg  
APPLICANT: Prydz, Hans Peter Blankenborg  
APPLICANT: Prydz, Hans Peter Blankenborg  
TITLE OF INVENTION: PSKH-1 Ribozymes and Uses in Disease





; CLONE: g1245391

US-09-016-434-1098

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Query Match          8.28;   Score 181.4;   DB 4;   Length 423;
Best Local Similarity 75.28;   Pred. No. 3.2e-31;
Matches 261;   Conservative 0;   Mismatches 41;   Indels 45;   Gaps 1;

QY 1241 CCACCGCGCTCCGCGCACCAACCATGGGCTGGTGAACAAAGCAAGAGTTTACTCAACA 1300
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Db 5 CCATCTCACCACCATGCTGGCCACACGGAATTTCTAGCAGCCAGAGTTTACTCAACA 64

QY 1301 AGAAGCAGATGGAGTCAAGCCCGACAGCAAGTACCAAAACAGTGCAGCGGCCACCA 1360
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Db 65 AGAAGCAGATGGAGTCAAGCCCGACAGCAAGTACCAAAACAGTGCAGCGGCCACCA 124

QY 1361 GCCCCAAAGGAGCGCTTCCCTGCGCGCCCTGGAGCCTCAACACCGCTCATTCATACC 1420
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Db 125 GCCCCAAAGGAGCGCTTCCCTGCGCGCCCT----- 155

QY 1421 CAGTGCAGGGATTAAAGAGTCTTCTGACAGTGCCTAATACCAATAGAGGATGAAGAG 1480
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Db 156 -----GGAGTCTTCTGACAGTGCCTAATACCAATAGAGGATGAAGAG 199

QY 1481 CTAAGCCCGGAGCAGAGATCATTAAGACACGAGCAGCTCATGAGGCGGTCAACA 1540
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Db 200 CTAAGCCCGGAGTCAAGAGATCATTAAGACACGAGCAGCTCATGAGGCGGTCAACA 259

QY 1541 ACGGTGACTTTGAGCGCTTACGCATTTACTTCGAGAAGCTGTGGGC 1587
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Db 260 ACGGTGACTTTGAGCGCTTACGCAGAAATCTGTGACCCAGGCTGACC 306
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## RESULT 14

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US-09-800-960-3
; Sequence 3, Application US/09800960
; Patent No. 6387677
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01158
; CURRENT APPLICATION NUMBER: US/09/800,960
; CURRENT FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 62804
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(62804)
; OTHER INFORMATION: n = A,T,C or G
US-09-800-960-3
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Query Match          7.88;   Score 174;   DB 4;   Length 62804;
Best Local Similarity 83.28;   Pred. No. 5.8e-29;
Matches 198;   Conservative 0;   Mismatches 40;   Indels 0;   Gaps 0;

QY 1580 TGTGCGCCAAAGAACGACGACCGATCCACAGCAGCCATCTGAAACACACACGTCACGTC 1639
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Db 59857 TCTGTGCCAAGAACGACGACCGATCCATACCCACCATCTTAACCCACGCTCCACGTGA 59916

QY 1640 TTGAGAGATGCGCGCTTGATCGCTTACATCCGCTCACAGTACATGACGGGACG 1699
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Db 59917 TTGGGAGGACGACGCTGTGATCCGCTACATCCGCTCACCCAGTACATGACGGGACG 59976

QY 1700 GCGGCGCGCGACGACGCTGTGAGGAGACCGCGGTGGCACCGCGCGGACGCAAGT 1759
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QY 1760 GGCAGAACGTCGACTTCCACTGCTCGGGCGCGCTGTGGCCCGCTGTCAGTGAAACCA 1817
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Db 60037 GGCTCAATGTCCACTATCACTGCTCAGGGGCCCTGCCGACGCTGCAGTAGCTCA 60094
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RESULT 15
US-09-579-664B-3
; Sequence 3, Application US/09579664B
; Patent No. 6514719
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
; FILE REFERENCE: 2923-A
; CURRENT APPLICATION NUMBER: US/09/579,664B
; CURRENT FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1694
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-579-664B-3
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Query Match          7.88;   Score 173.2;   DB 4;   Length 1694;
Best Local Similarity 52.08;   Pred. No. 3.1e-29;
Matches 438;   Conservative 0;   Mismatches 398;   Indels 6;   Gaps 2;

QY 301 TACCAGCTCTACGAGGATATGGCAAGGGGGCTTTCTCTGTGTCGCGAGCTGTGTCAAG 360
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Db 309 TTCGAGTTCAAGGAGACCTCGGAATCGGGCCCTTTCTGAGTTGTTTATAGCGAGGAG 368

QY 361 CTCCTGACCGGCCATGAGTATGCACCAAGATCATCAACCAAGAGCTGTCAGCCAGA 420
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Db 369 AAAGCTACTGGGAAGCTCTTCGCGTGAAGTGCATCCCGAAGAGCGCTGAAGGGGAG 428

QY 421 GATCACCAAGAGCTGGAGAGAGAGCTCGGATCTGCGCGCTTCTGAAGCATTCACACATC 480
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
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QY 481 GTGCGTCTCCAGACAGCATCTCCGAGAGGGCTTCACCTACCTGCTCTGTGATCGTGC 540
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Db 606 AGCACTCTCATCGCCAGGTCTCTGGATGCGGTATCTATCTATCTATCTCCACAGATGGCAT 665

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QY 721 AAGCTGGCAGACTTCGCGCTAGCTATCGAGGTGAGGGGGACGACGAGCATGTTTGGT 780
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QY 901 TTCTGGGAGGAGGACGACGACAGCTGTACCGAGAGATCAAGGCTGGTGGCTTACGCTTC 960
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Db 903 TTTTATGATGAATGACTCGAGAGCTGTTTGAACAGATCTCTCAAGCAGATATGAGTTT 962
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QY	961	CGTCCCTCGTAGTGGGACACGGCTACTCTCTGAAGCCAAACCTCATCAACAGATCGT	1020
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QY	1021	ACCATCAACCCCTGCCAAGCCGNCACAGCCCATGAGCCCTGAAGCACCCGTGGGTCTGC	1080
Db	1023	GAGAAAGACCCCAATATAAGATACATTGTGAGCAGGACGCTCGACACCCATGGATTGCT	1082
QY	1081	CAACGGTCCACGGTAGCATCCATGATGSCACAGACAGGAGACTGTGGAGTGTCTGAAAAAG	1140
Db	1083	GGTGACACAGCCCTTAGCAAAAACATTACAGAACTGTCTCAGTCCCAAGATCCGAGAGAT	1142
QY	1141	TT	1142
Db	1143	TT	1144

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Job time : 155 secs

GenCore version 5.1.6  
 Copyright (c) 1993 - 2003 CompuGen Ltd.  
 OM nucleic - nucleic search, using sw model  
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 (without alignments)  
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Title: US-09-820-790B-1  
 Perfect score: 2218  
 Sequence: 1 CGGCGCGCGCGCGCGCGG.....taggtgtcccggtgtggtg 2218

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0  
 Searched: 1731049 seqs, 1297405648 residues

Total number of hits satisfying chosen parameters: 3462098

Minimum DB seq length: 0  
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 Maximum Match 100%  
 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	2218	100.0	2218	US-09-820-790-1
2	785.6	35.4	3705	US-10-044-090-227
3	769.4	34.7	2061	US-10-096-960-1
4	721.4	32.5	5637	US-09-917-800A-1537
5	619.2	27.9	1500	US-10-354-358-87
6	619.2	27.9	1500	US-10-393-892-1
7	619.2	27.9	1500	US-10-394-382-1
8	610.2	27.5	1551	US-09-925-299-210
9	610.2	27.5	1551	US-09-925-299-210
10	435.2	19.6	488	US-09-918-995-509
11	395.8	17.8	28438	US-09-820-790-3
12	313.5	14.1	474	US-09-918-995-316
13	282.2	12.7	556	US-09-918-995-26755
14	260.2	11.7	476	US-09-918-995-26869
15	247	11.1	461	US-09-918-995-410
16	235	10.6	435	US-09-764-868-184
				Sequence 1, Appli
				Sequence 227, App
				Sequence 1, Appli
				Sequence 1537, Ap
				Sequence 87, Appl
				Sequence 1, Appli
				Sequence 210, App
				Sequence 509, App
				Sequence 3, Appli
				Sequence 316, App
				Sequence 26755, A
				Sequence 26869, A
				Sequence 410, App
				Sequence 184, App

c	17	232.8	10.5	455	10	US-09-880-107-790	Sequence 790, App
	18	214	9.6	1480	12	US-10-204-041-9	Sequence 9, Appli
	19	202.8	9.1	981	12	US-10-090-002-1	Sequence 1, Appli
	20	202.8	9.1	1372	10	US-09-817-181-1	Sequence 1, Appli
	21	202.8	9.1	1372	14	US-10-300-828-1	Sequence 1, Appli
	22	185.8	8.4	1282	12	US-09-769-970-12	Sequence 12, Appl
	23	185.2	8.3	1349	11	US-09-988-462-20	Sequence 20, Appl
	24	184	8.3	1383	11	US-09-935-464-2	Sequence 2, Appli
	25	184	8.3	1383	14	US-10-125-835-2	Sequence 2, Appli
	26	184	8.3	1738	11	US-09-935-464-4	Sequence 4, Appli
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	28	174	7.8	62804	13	US-10-096-960-3	Sequence 3, Appli
	29	173.2	7.8	1694	12	US-10-355-975-3	Sequence 3, Appli
	30	171.6	7.7	1947	14	US-10-024-036B-6	Sequence 6, Appli
	31	171.6	7.7	2454	10	US-09-992-481-3	Sequence 3, Appli
	32	171.6	7.7	2454	12	US-10-434-034-3	Sequence 3, Appli
	33	171.6	7.7	2824	10	US-09-992-481-5	Sequence 5, Appli
	34	171.6	7.7	2824	12	US-10-434-034-5	Sequence 5, Appli
	35	171.6	7.7	3579	14	US-10-024-036B-4	Sequence 4, Appli
	36	171.2	7.7	1733	14	US-10-037-270-526	Sequence 526, App
	37	171.2	7.7	1772	14	US-10-024-036B-1	Sequence 1, Appli
	38	170.6	7.7	1458	12	US-09-735-138-5	Sequence 5, Appli
	39	167.6	7.6	1074	14	US-10-024-036B-3	Sequence 3, Appli
	40	167.6	7.6	1578	9	US-09-835-788A-6	Sequence 6, Appli
	41	167.6	7.6	1578	12	US-10-175-042-6	Sequence 6, Appli
	42	164.6	7.4	501	11	US-09-918-995-25048	Sequence 25048, A
	43	162	7.3	753	9	US-09-910-943-333	Sequence 333, App
	44	159.8	7.2	2224	14	US-10-059-585-11	Sequence 11, Appl
c	45	153.4	6.9	478	11	US-09-918-995-22184	Sequence 22184, A

## ALIGNMENTS

RESULT 1  
 US-09-820-790-1  
 ; Sequence 1, Application US/09820790  
 ; Publication No. US20030140354A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SHAO, Wei et al.  
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
 ; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
 ; TITLE OF INVENTION: THEREOF  
 ; FILE REFERENCE: CL001204  
 ; CURRENT APPLICATION NUMBER: US/09/820,790  
 ; CURRENT FILING DATE: 2001-03-30  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 2218  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-09-820-790-1

Query Match	100.0%	Score 2218;	DB 12;	Length 2218;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2218;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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QY	61	GCSCGCTCTCGCGAGACGAGCAGACATCTCGCTGCTCGCGCGCGCGCGCGC	120	
Db	61	GCSCGCTCTCGCGAGACGAGCAGACATCTCGCTGCTCGCGCGCGCGCGC	120	
QY	121	CGAGCCGCGCGCGCGCGTTCGCGCGCGCGCGCGCGGTCTCCCGCGCGCGCGGTTC	180	
Db	121	CGAGCCGCGCGCGCGCGTTCGCGCGCGCGCGCGCGGTCTCCCGCGCGCGCGGTTC	180	
QY	181	GCSCGCTCTCGCGAGCGCGCGCGGTTCGCGCGCGCGCGCGCGGTTCGCGCGCGCG	240	
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QY	1088	CCACGGTAGCATCCATGATGACACAGACAGAGAGACTGTGAGTGTCTGAAAAGCTTCATG	1147
DB	909	CCACGGTGGCATCCATGATGATCGTTCAGAGAGACTGTGAGTGTCTGAAAAGCTTCATG	968
QY	1148	CCAGGAGAAAGTCTCAAGGGAGCCATCTCTACCAACCATGCTGCCACACAGGAATTTCTCAG	1207
DB	969	CCCGGAGAAATCTGAGGGTGCATCTCTACGACCATGCTTGTCTCCAGGAATTTCTCAG	1028
QY	1208	TGGCGACAGACAGACACCGCTCCGCGCCACAATGTCACCGCGGCTTCGCGGACCAACATGG	1267
DB	1029	CTGCGAAA-----AGCCTATTGAACAAGAAGTCGGGATGGC-----G	1064
QY	1268	GGCTGGTGGACAGCCCAAGAGTTTACTCTACAAGAAAGCAGATGGAGTCAAGCCCCAGA	1327
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QY	1328	CGAATAGCACCAAAACAGTGCACGCCGCCACCAAGCCCAAGAGGACGCTTCCTCTTGGCG	1387
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US-10-096-960-1			
; Sequence 1, Application US/10096960			
; Publication NO. US20020132325A1			
; GENERAL INFORMATION:			
; APPLICANT: YE, Jane et al.			
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC			
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES			
; TITLE OF INVENTION: THEREOF			
; FILE REFERENCE: CL001158D1V			
; CURRENT APPLICATION NUMBER: US/10/096,960			
; CURRENT FILING DATE: 2002-03-14			
; PRIOR APPLICATION NUMBER: 09/800,960			
; PRIOR FILING DATE: 2001-03-08			
; NUMBER OF SEQ ID NOS: 4			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 1			
; LENGTH: 2061			
; TYPE: DNA			
; ORGANISM: Homo sapien			

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Qy	1175	TCACCAACATGCTGGGCCAACAGGAATTTCTAGTGGGCAGACAGACACCGCTCGGGCCA	1234
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Qy	1235	CAATGTCCACGGCGCCTCCGGC-----	1257
Db	1086	CGCTGCGCGAGCGCGCGCGCTGCGCGGGCAAGCTGCCAAAGCCTATTGAACAAGA	1145
Qy	1258	-----ACCAACATGGGCTGGTGACCAAG	1282
Db	1146	AGTCGGATGCGGTGTCAGAAAGGAAGTCGAGTTCCAGCGTGCACTAATGGAGCCAC	1205
Qy	1283	CGAAGATTCTACTACACAGAAACGAGATGGAGTCAAGCCCGACAGCAAGTAGCACACAAA	1342
Db	1206	AAACCACTGTGTTACACACGCTACAGATGGGATCAAGGGCTCCACAGAGAGCTGCACA	1265
Qy	1343	ACAGTGCAGCGCCACACAGCCCAAGAGGACGCTCTCTCTGCGCGCCTGGAGCCTCAA	1402
Db	1266	CGACCAACAGAGATGASGACCTCAA-----GCTGCCCGCTCCGCACCTGGGATGGCAG	1322
Qy	1403	CGACCGTTCATCCATAACCCAGTGGACCGGATTAAGAGATCTTCTGACAGTGCCCAATACCA	1465
Db	1321	CTCGGTGCTGAAGGACGGAGCTCCGGGACAGACAGACAGCCCTCTCGAGGCATGGCAGCC	1380
Qy	1463	CGATAGAGGATGAAGACGCTAAAGC-----CCGGAACAGGAGATCATTTAAGACCGAGCA	1520
Db	1381	CGCGCTCTCTCTGCTCTCTCGACCTCGGAACAGGAGATCATTAAGATTACAGACA	1440
Qy	1521	GCTCATCGAGCGCGTCAACACGGTGTGACTTTGAGGCTACGC-----	1566
Db	1441	GCTGATTGAAGCCATCAACAATGGGGACTTTGAGGCTTACACGAAGATTTGTGATCAGG	1500
Qy	1563	-----	1563
Db	1501	CCTCACTTCCTTGAAGCCTGAGGCGCTTGTGTAACCTCGTGGAGGGATPGGATTTCCATAA	1566
Qy	1563	ATTCTACTTTCAGAAACCTGCTGGCCCAAGACAGCAAGCGGATCCACAGCACTCTGTAA	1622
Db	1561	GTTTTCTTCTTGTAGAACTCTCTCTCCACAGACAGCAAGCCTATCCATACCACTCTAA	1622
Qy	1623	CCACACGTGCAGCTCAATTGGAGAGATGCGCGCTGCATCGTTCATATCCGGGCTCACGA	1681
Db	1621	CCACACCTCCACGTGATTGGGAGGAGCGAGCGTCATCGCTCATATCCCGCTCACCA	1681
Qy	1683	GTACATTGACGGGACGGGCGGCGCCGACACCGCACTCTGAGGAGACCGCGCTGGCA	1744
Db	1681	GTACATCGAGGGCGGGCTCGGCCTCGCACGACGAGTCAGAAAGAGACCGGGGCTGGCA	1744
Qy	1743	CGCGCGCACGGCAAGTGGCAGAAAGTGCATTCCTCATGCTCGGGCGGCGCTGTGGCGCC	1800
Db	1741	CGCTGGGATGGCAAGTGGCTCAATGTCCACTATCATCTGCTCAGGGGCGCCTCGCGCAC	1800
Qy	1803	GTCGAGTGAAGCCA	1817
Db	1801	GCTGCAGTGAAGTCA	1815

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US-09-917-800A-1537
; Sequence 1537, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,
; CURRENT FILING DATE: 2001-07-31

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Db	643	AAATTTGCTTTTACGTAGCAAAATCCAAAGGAGCAGCTGTGAACTGGCAGACTTCGGCTTA	702
QY	742	GCTATCGAGGTCCAGGGGACACGAGGATGGTTTGGTTTTCGTGTGGCACACACAGGCTAC	801
Db	703	GCCATAGAAAGTTCAGGCGACACGAGCGTGGTTTGGTTTGGTGGCACACTGGGTAT	762
QY	802	CTGTCCCTTGAGGTCCTTTCGAAAGAGGCGTAGGCAAGCCTGTGGACATCTGGGCACTGT	861
Db	763	CTTTCTCCAGAAAGTCCTACGTAAAGATTCCTTATGAAAAACCAAGTGGACATGTGGCACTGT	822
QY	862	GGGTGTGCTCTGATCATCTGCTCGTGGGCTACCCACCCCTTCTGGGACGAGGACACAGCAC	921
Db	823	GGCGTATCTCTGATCTTCTGTGGTGGATACCCACCCCTTCTGGGATGAAATCAGCTGT	882
QY	922	AAGCTGTATCCAGCAGATCAAGGCTTGGTCTATGACTTCCGGTCCCTCGAGTGGACACC	981
Db	883	AGACTGTATCAGCAGATCAAGGCTTGGAGTACCCACCCCTTTCATCACCAGAATGGACACA	942
QY	982	GTCACTCTCTGAGGCCAAAAAACCTCATCAACCAGATGCTGACATCAACCTGCCAAGCGC	1041
Db	943	GTGACACCTTGAAGCAAAAGACCTCATCAAAAAATGCTGACCATCAACCCCTGCCAAAGCG	1002
QY	1042	ATCACAGCCATGAGGCGCCTGAAGCACCCGTGGGTCTGCCAACGCTCCACGATGATCATCC	1101
Db	1003	ATCACAGGCTCTGAGGCGCTGAAACACCCCATGATGCTGCAAGCTTCTACTGTTCGCTCC	1062
QY	1102	ATGATGCACAGCAGAGACTTGGAGTGTCTGAAAAATGTCATGCCAGGAGAAGCTC	1161
Db	1063	ATGATGCACAGCAGAGACTTGAATGCTTGAAGAAATTAATGCTCGACGGAATTTG	1122
QY	1162	AAGGAGGCCATCCTCACCACCATGCTGGCCACACGGAATTTCTCAGTGGGCAGACAGACC	1221
Db	1123	AAGGTTGCCATCTTGACAACTATCTGGCTACGAGAAATTTTCAG-----CAGCCA	1174
QY	1222	ACCGCTCCGGCCCAATGTCCACCGCGCGCTCCGGCACACCATGGGGCTGTGTGAACAA	1281
Db	1175	AGAGTTTGTGAAGAAACCGGATGGGATAAGATAAACAACAAGACCAACGCTGGTAACCA	1234
QY	1282	GCCAGAGTTTACTCAACAAGAAAGCAGATGGAGTCAAGCCCCAGACGAATAGCACCAA	1341
Db	1235	GCCCCAA----AGAAAAATTTCTTACCCCGCGCTGGAGCCCCAAACTACTGTATCCAC	1290
QY	1342	AACAGTGCAGCGCCACACGCCCCAAAGGACGCTTCCTCTGCGCGCTGGAGCGCTCAA	1401
Db	1291	AACCGTATGGAACAAGGAGTCAACTGAGA---GCTCAAAATACACCATTTAGGATGAA	1347
QY	1402	ACCACCGTCAATCATCAACCCAGTGGACGGGATTAAGGAGTCTCTGACAGTGCATACCC	1461
Db	1348	GACGTGAAGACGAGAAACGACAGATCATCAAGTCACTGAGCAGCTGATGAGCTATC	1407
QY	1462	ACCATAGAGATGAAGACGCTAAAGCCCGGAGACGAGAGATCATTAAGACACGGAGCAG	1521
Db	1408	AACAATGGGACTTCGAGGCTTACAGAAAAATCTGTGATCCAGGCGCTACTGCTTTGAA	1467
QY	1522	CTCATCGAGCGCTCAACAAGGTGACTTTTGGGCT---ACGCATTCACTTCGAGAAC	1578
Db	1468	CCGAGCAFTTGGCAACTTATGGAAGGATGGACTTTCAGATTCACTTTGAAAT	1527
QY	1579	CTGTGTCGCAAGAAGCAGACCGCATCCACAGACCATCTCTGAACCCACACCTGCACGTC	1638
Db	1528	GCTTTGCCAAAAATCAATAAACCAATCCACACTATCATCCTGAACCCCTCAGCTACACCTG	1587
QY	1639	ATTGGAGAGATGCGCGCTGATCGCTTACATCCGGCTCAGCGAGTACATGACGGGAC	1698
Db	1588	GTAGGGATGATGACGCGCTGATAGCATATATTCGGCTCACACAGTACATGATGGAAT	1647
QY	1699	GGCGGCGCGCACACGACGCTGTGAGGAGACCGCGTGTGGCACCGCCGACGACGCAAG	1758
Db	1648	GGAATGCCAAAGCAATGCAATCAGAAAGACTTCGAGTGTGGCACCGCGTATGGGAG	1707
QY	1759	TGGCAAGATGCACTTCCACTGCTGGGCGCGCGCTGTGGCCCGCGCTGAC	1809

[illegible]



Db 1708 TGGCAGAAATATTCACCTTTCATCGTTCGGGGTCCCCAACAGTCCCCATCAAG 1758

	DB	181	GAGCTAGAATCGCCGCTTTTGGACCAACCCTAATAATTGTGGACTTCATGATAGCATTA	24
	QY	502	TCCGAGGAGGGCTTCACCPACTGGTCTTGCGATCGTGCACCTGGTGGGAGCCTTTTGAA	561
	DB	241	TCAGAAGAGGGCTTCACCTACTTGGTCTTTGATTTAGTTACTGTGAGGTGAAGCTTTTGA	300
	QY	562	GACATGTGGCGAGAGTAGTACAGCGAGGCTGATGCCAGTCACTGTATCCACGATC	621
	DB	301	GCATAGTGGCAGAGACTACAGTGAAGCTGATGCCAGTCACTGTATCCACGATC	360
	QY	622	CTGGAGGCGCTTCCATTGTTCACAAATGGSGCTGCTCCACAGAGAACCTCAAGCCGGAG	681
	DB	361	CTAGAAAGTGTTAATCATTTGTCACTAAATGGCATAGTTCACAGGGACCTGAAGCCTGAG	420
	QY	682	AACCTGCTTCTGGCCAGCAGTGAAGAGGGCTGCAGTGAAGCTGGCACACTCTGGGCTA	741
	DB	421	AATTTGCTTTTGTAGTAGCAAAATCCAAGGGAGCAGCTGTGAATTTGGCAGACTTTGGCTTA	480
	QY	742	GCTATCGAGTGCAGGGGACACACAGAGCATGGTTTTGCTTTCGCTGSCACACAGGCTAC	801
	DB	481	GCCATAGAAGTTCAGGGGACACAGCGCTGGTTTGGTTTGTCTGCTGSCACACCTGGATAT	540
	QY	802	CHGTCCCTGAGGTCCCTTCGCAAGAGCGCTATGCCAGAGCCTGTGCACATCTGGGCATGT	861
	DB	541	CTTTCTCCAGAAGTTTACGTAAAGATCCCTTATGAAAAGCCAGTGGATATGTTGGGCATGT	600
	QY	862	GGGGTGATCTGCTGACATCCCTGCTGGGGCTACCCACCCCTTCTGGGACGAGGACACAC	921
	DB	601	GGTGTCATCTCTATATCTACTTTGGGGTATCCACCCCTCTGGGATGAAGACCAACAC	660
	QY	922	AAGCTGTACAGCAGATGAAGCTGTGGTGCCTATGACTTCCCGTCCCCTGAGTGGGACAC	981
	DB	661	AGACTCTATCAGCAGATGAAGCTTGAAGCTTATGATTTTCCATCACCAGAAATGGGACAG	720
	QY	982	GTCACTGCTGAAGCAAAAAACCTCATCAACAGATGCTGAOCATCAACCCCTGCCAAGCGC	104
	DB	721	GTGACTCTGAAGCCAAAGACCTCATCAATAAATGCTTACTATCAACCCCTGCCAAGCGC	780
	QY	1042	ATCAGAGCCCATGAGGCCCTGAAGCACCCCTGGGCTGCGCAACGCTCCAGGTAGCATCC	110
	DB	781	ATCAGAGCCTCAGAGGCACTGAAGCACCCCATGGATGTCTCAACGTTTCTGCTTCTTCC	840
	QY	1102	ATGATGCACAGACGAGGACTGTGGAGTGTCTCAAAAGTTCAATGCCAGGAGAAAGCTC	116
	DB	841	ATGATGCACAGACGAGGACTGTAGCTTGAAGAAATTTATGCTAGAGAAACA	900
	QY	1162	ARGGGAGCCATCTTCACCAACATGCTGGCCACACGGAATTTCTCAGTGGGCA	1213
	DB	901	ARGGGTGGCATCTTGACAACTATGCTGGCTACAAGGAATTTCTCAGCAGCCA	952

RESULT 6  
US-10-393-892-1  
; Sequence 1, Application US/10393892  
; Publication No. US20030186302A1  
; GENERAL INFORMATION:  
; APPLICANT: WANG, YIXIN  
; TITLE OF INVENTION: COLORECTAL CANCER DIAGNOSTICS  
; FILE REFERENCE: CDS 267 US NP  
; CURRENT APPLICATION NUMBER: US/10/393,892  
; CURRENT FILING DATE: 2003-03-21  
; PRIOR APPLICATION NUMBER: 60/368,798  
; PRIOR FILING DATE: 2002-03-29  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1500  
; TYPE: DNA  
; ORGANISM: human

US-10-393-892-1

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Query Match      27.9%; Score 619.2; DB 12; Length 1500;
Best Local Similarity 78.2%; Pred. No. 2.2e-153;
Matches 744; Conservative 0; Mismatches 208; Indels 0; Gaps 0;

QY 262 ATGGCCACACAGGCTGACCTGCACCCGCTTCACCGACGAGTACAGCTCTACGAGATAT 321
Db 1 ATGGCTTCGACCAACCACTGCACCGCTTCACCGACGAGTATCAGCTTTTCGAGGAGCTT 60
QY 322 GGCAGAGGGGCTTTCTCTGTTGTCGACGCTGTGTCAGGCTCTCAGCCGCTCAGATAT 381
Db 61 GGAAGGGGCACTTCTAGTGGTCAGAGATGTATGAAATCTCTAGTGCACAGATAT 120
QY 382 GCAGCCAGATCATCAACACCAAGAGCTGTGACGACAGATCACCAGAGCTTGGAGAGA 441
Db 121 GCTGCCAAATATCAACACCAAGAGCTTCTGCTAGGATCATCAGAACTAGAGA 180
QY 442 GAGCTCGGATCTGCGGCTTCTGAGCATTCACATCGTCCGCTCCACGACGATC 501
Db 181 GAAGCTAGATCTGCGGCTTCTGAGCATTCACATCGTCCGCTCCACGACGATAT 240
QY 502 TCGAGAGGGGCTTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 561
Db 241 TCAGAGAGGGGCTTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 562 GACATTTGTCGACGAGAGTACTACAGGAGGCTGTAGCCAGTCACTGTATCCAGAGATC 621
Db 301 GACATAGTGGCAAGAGATATCACTAGTGAAGCTGTAGCCAGTCACTGTATCCAGAGATC 360
QY 622 CTGAGAGGGGCTTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 681
Db 361 CTAGAGAGGGGCTTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 682 AAGCTGCTGTCGACGAGAGTACTACAGGAGGCTGTAGCCAGTCACTGTATCCAGAGATC 741
Db 421 AATTTCTGAGAGGGGCTTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 742 GCTATCGAGGTGCAAGGAGGCTGTAGCCAGTCACTGTATCCAGAGATC 801
Db 481 GCATAGAGAGGGGCTTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 802 CTGTCCTGTCGAGAGAGTACTACAGGAGGCTGTAGCCAGTCACTGTATCCAGAGATC 861
Db 541 CTGTCCTGTCGAGAGAGTACTACAGGAGGCTGTAGCCAGTCACTGTATCCAGAGATC 600
QY 862 GGGGTGATCTGTCGAGAGTACTACAGGAGGCTGTAGCCAGTCACTGTATCCAGAGATC 921
Db 601 GGTGTCATTTCTGAGAGTACTACAGGAGGCTGTAGCCAGTCACTGTATCCAGAGATC 660
QY 922 AAGCTGTCGAGAGAGTACTACAGGAGGCTGTAGCCAGTCACTGTATCCAGAGATC 981
Db 661 AGACTCTATCAGAGAGTACTACAGGAGGCTGTAGCCAGTCACTGTATCCAGAGATC 720
QY 982 GTACCTCTGAGAGAGTACTACAGGAGGCTGTAGCCAGTCACTGTATCCAGAGATC 1041
Db 721 GTGACTCTGAGAGAGTACTACAGGAGGCTGTAGCCAGTCACTGTATCCAGAGATC 780
QY 1042 ATCAGAGCCATGAGGCGCTGAGAGAGGCTGTAGCCAGTCACTGTATCCAGAGATC 1101
Db 781 ATCAGAGCCATGAGGCGCTGAGAGAGGCTGTAGCCAGTCACTGTATCCAGAGATC 840
QY 1102 ATGATGACAGAGAGGCTGTAGGAGGCTGTAGGAGGCTGTAGGAGGCTGTAGGAGGCT 1161
Db 841 ATGATGACAGAGAGGCTGTAGGAGGCTGTAGGAGGCTGTAGGAGGCTGTAGGAGGCT 900
QY 1162 AAGGAGGAGGCTGTAGGAGGCTGTAGGAGGCTGTAGGAGGCTGTAGGAGGCTGTAGGAGGCT 1213
Db 901 AAGGAGGAGGCTGTAGGAGGCTGTAGGAGGCTGTAGGAGGCTGTAGGAGGCTGTAGGAGGCT 952

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RESULT 7

US-10-394-382-1

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; Sequence 1, Application US/10394382
; Publication No. US20030186303A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Yixin
; TITLE OF INVENTION: COLORRECTAL CANCER DIAGNOSTICS
; FILE REFERENCE: CDS 266 US NP
; CURRENT APPLICATION NUMBER: US/10394,382
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,687
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1500
; TYPE: DNA
; ORGANISM: human
US-10-394-382-1

Query Match      27.9%; Score 619.2; DB 12; Length 1500;
Best Local Similarity 78.2%; Pred. No. 2.2e-153;
Matches 744; Conservative 0; Mismatches 208; Indels 0; Gaps 0;

QY 262 ATGGCCACACAGGCTGACCTGCACCCGCTTCACCGACGAGTACAGCTCTACGAGATAT 321
Db 1 ATGGCTTCGACCAACCACTGCACCGCTTCACCGACGAGTATCAGCTTTTCGAGGAGCTT 60
QY 322 GGCAGAGGGGCTTTCTCTGTTGTCGACGCTGTGTCAGGCTCTCAGCCGCTCAGATAT 381
Db 61 GGAAGGGGCACTTCTAGTGGTCAGAGATGTATGAAATCTCTAGTGCACAGATAT 120
QY 382 GCAGCCAGATCATCAACACCAAGAGCTGTGACGACAGATCACCAGAGCTTGGAGAGA 441
Db 121 GCTGCCAAATATCAACACCAAGAGCTTCTGCTAGGATCATCAGAACTAGAGA 180
QY 442 GAGCTCGGATCTGCGGCTTCTGAGCATTCACATCGTCCGCTCCACGACGATC 501
Db 181 GAAGCTAGATCTGCGGCTTCTGAGCATTCACATCGTCCGCTCCACGACGATAT 240
QY 502 TCGAGAGGGGCTTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 561
Db 241 TCAGAGAGGGGCTTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 562 GACATTTGTCGACGAGAGTACTACAGGAGGCTGTAGCCAGTCACTGTATCCAGAGATC 621
Db 301 GACATAGTGGCAAGAGATATCACTAGTGAAGCTGTAGCCAGTCACTGTATCCAGAGATC 360
QY 622 CTGAGAGGGGCTTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 681
Db 361 CTAGAGAGGGGCTTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 682 AAGCTGCTGTCGACGAGAGTACTACAGGAGGCTGTAGCCAGTCACTGTATCCAGAGATC 741
Db 421 AATTTCTGAGAGGGGCTTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 742 GCTATCGAGGTGCAAGGAGGCTGTAGCCAGTCACTGTATCCAGAGATC 801
Db 481 GCATAGAGAGGGGCTTCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 802 CTGTCCTGTCGAGAGAGTACTACAGGAGGCTGTAGCCAGTCACTGTATCCAGAGATC 861
Db 541 CTGTCCTGTCGAGAGAGTACTACAGGAGGCTGTAGCCAGTCACTGTATCCAGAGATC 600
QY 862 GGGGTGATCTGTCGAGAGTACTACAGGAGGCTGTAGCCAGTCACTGTATCCAGAGATC 921
Db 601 GGTGTCATTTCTGAGAGTACTACAGGAGGCTGTAGCCAGTCACTGTATCCAGAGATC 660
QY 922 AAGCTGTCGAGAGAGTACTACAGGAGGCTGTAGCCAGTCACTGTATCCAGAGATC 981
Db 661 AGACTCTATCAGAGAGTACTACAGGAGGCTGTAGCCAGTCACTGTATCCAGAGATC 720
QY 982 GTACCTCTGAGAGAGTACTACAGGAGGCTGTAGCCAGTCACTGTATCCAGAGATC 1041
Db 721 GTGACTCTGAGAGAGTACTACAGGAGGCTGTAGCCAGTCACTGTATCCAGAGATC 780

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QY 1042 ATCAAGCCATGAGGCCCTGAGACCCCGTGGGTGCGCAACGCTCCACGGTAGCATCC 1101
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Db 781 ATCAAGCCTCAGAGGCACTGAAGCAACCCATGGATCTGTCAAGCTTCTACTGTTCC 840
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QY 1102 ATGATGCACAGAGGAGACTGGGAGTGTCTGAAAAGTTCAATCCAGGAGAAAGTC 1161
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Db 841 ATGATGCACAGAGGAGACTGTAGACTGTGTGAGAAATTAATCTAGAGAAACTA 900
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QY 1162 AAGGAGCCATCCTCACACCATGTGCGCACAGGAATTCACAGTGGCA 1213
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Db 901 AAGGTGCCATCTTGACAACATGCTGGCTACAGGAATTTCTCAGCACCA 952
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RESULT 8
US-09-925-299-210
; Sequence 210, Application US/09925299
; Patent No. US2002005627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 210
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (760)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1543)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1544)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1545)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1546)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-210

Query Match 27.5%; Score 610.2; DB 9; Length 1551;
Best Local Similarity 78.0%; Pred. No. 5.2e-151;
Matches 744; Conservative 2; Mismatches 206; Indels 2; Gaps 1;

QY 262 ATGCCACACCGTCACTGACCCGCTTCACCGACGAGTACAGCTCTACGAGNTATT 321
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Db 489 ATGGCTTCACACCAACCTGCACGAGTTCACGGACGAGTACAGCTTTCGAGGAGCTT 548
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QY 322 GGCAAGGGGGCTTCTCTGTGTGTCGACGCTGTGTCAAGCTCTGCACCCGCCATGATAT 381
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Db 549 GGAAGGGGGCTTCTCTGTGTGTCGACGAGTGTATGAAATTCCTACTGGACAGAAATAT 608
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QY 392 GCAGCCAGATCATCAACACAGAGAGCTGTGAGCCAGAGATCACCAAGCTGGAGAGA 441
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Db 609 GCTGCCAAAATATCAACACAAAAGCTTTCTGTAGGGATCATCAGAAACTAGAAAGA 668
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QY 442 GAGCTGGATCTGCGGCTTCTGAAGCATTCACATCGTGTCTCCACAGCAGCATC 501
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Db 669 GAAGCTAGATCTGCGGCTTTTGAAGCACCTTAATATGTGCGACTTCATGATAGCATAT 728
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QY 502 TCCAGGAGGGCTTCCACTACT--GGTCTTGTGACTGGTCACTGGTGGGAGGCTCTTTG 559
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Db 729 TCAGAGAGGGCTTCTCACTACTTGGTGGTNGATTAAGTTACTGGAGGTGAACCTTTTG 788
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QY 560 AAGACATTTGGCGAGAGAGTACTACAGCAGGCTGATCCAGTGCACGTATCCACAGA 619
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Db 789 AAGACATAGTGGCAAGAGAACTACTACAGTGAAGCTGATCCAGTCAATGCAATCAGACA 848
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QY 620 TCCTGGAGGGCTTCTCCATTTGTCACCAATGGGGTCTGCCACAGAGACCTCAAGCCGG 679
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QY 680 AAGACCTGCTTCTGGCCAGCAAGTCAAGAGGGCTCAGTGAAGTGCAGACTTGGGCC 739
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Db 909 AAGATTTGCTTTAGCTAGCAATCCAGGAGCAGCTGTGAATTCGACAGCTTTGGCT 968
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QY 740 TAGCTATCGAGGTGCAGGGGACACAGCAGCATGTTGGTTTCCTGGCACACACAGGT 799
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Db 969 TAGCCATAGAAGTTCAAGGGGACCAGCAGGCTGTGGTTGTTTCTGGCACACCTGGAT 1028
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QY 800 ACCTGTCCCTGAGTCTTCGCAAGAGAGGCTATGGCAAGCCTGTGACATCTGGGCAT 859
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Db 1029 ATCTTTCTCYCARAAGTTTACGTAAAGATCCTTATGGAAGCCAGTGGATATGSGCAT 1088
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QY 860 GTGGGGTGATCCTGTATCATCTCTGTGTGGGCTACCCACCTTCTGGGACGAGACAGC 919
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Db 1089 GTGGTGCTCATCTCTATATTCTTACTTGTGGGGTATCCACCCTTCTGGGATGAAGCAAC 1148
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QY 920 ACAAGCTGTACACAGCAGATCAAGGCTGTGCTTACGTTCCGCTCCCTGAGTGGGACA 979
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Db 1149 ACAGACTCTATACAGCAGATCAAGGCTGGAGCTGTATGATTTCCATCACCAGATGGGACA 1208
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QY 980 CGGTACTCTCTGAAGCCAAAACCTCAATCAACAGAGTGTGAGTCCGCTCCCTGAGTGGGACA 1039
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Db 1209 CGGTACTCTCTGAAGCCAAAAGACCTCAATCAATAAATGCTTACTATCAACCTGCCAACC 1268
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QY 1040 GCATCAGAGCCCATGAGCCCTGAGGACCGGTGGGCTGCCAAGCTCCACGCTAGCAT 1099
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Db 1269 GCATCAGAGCCCTCAGAGGCACTGAAGCACCCTGATGATCTGCAAGCTTCTACTGCTT 1328
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1100 CCATGATGCACAGACAGGAGACTGTGGAGTGTCTGAAAAAGTTCAATCCAGGAGAGAAC 1159
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1329 CCATGATGCACAGACAGGAGACTGTAGACTGCTTTGAAGAAATTTAATGCTAGAGAAAC 1388
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1160 TCAGGAGGCGATCCTCACCACCATGCTGGCCACAGCAGGAATTTCTCAGTGGCA 1213
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1389 TAAGGGTGGCATCTTGACACTATGCTGGCTACAGGAATTTCTCAGCAGCCA 1442
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
US-09-925-299-210
; Sequence 210, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 210
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (760)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
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; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-316

Query Match      14.1%; Score 313.6; DB 11; Length 474;
Best Local Similarity 83.7%; Pred. No. 7.6e-73;
Matches 35; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY      741 AGCATATCGAGGTGCGAGGGGACGACGAGCATGTGTTTGCCTGSGCACACGAGCTA 800
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      51  ACCCATCGAAGTACAGGAGAGCAGCAGCCTGTGTTTGGTTTTCCTGGCACCCAGGTTA 110

QY      801 CCTGTCCCTCCTGAGTCCCTWTGCAAAAGAGCGGTATGGCAGCCTCTGGACATCTGGGCATG 860
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      111 CTTGTCTCTTTGAGGTCTCTTGAGGAAAGATCCCTATTGGAACACGTTGTGGATATCTGGGCTG 170

QY      861 TGGGGTGTACTCTGTACATCTCTGCTTGGGCTTACCCACCTTCTTGGAGCGAGGACCGACGA 920
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

171  CGGGGTCATCCCTGTAATATATCCCTCGGCGGGGCTATATCCCTCTGGGATGAGAGATCAGCA 230
QY  921  CAAGCTGTATACCAGCAGATCAAGGCTGGTGCCTATGACTTCCCGTCCCTCGAGTGGGACAC 980
      |||||
Db  231  CAAGCTGTATCAGCAGATCAAGGCTGGAGCTTATGATTCCCATCACCAGAATGGGACAC 290
      |||||
QY  981  CGTCACTCTCTGAGCCGCGGAAAACCTCATCAACAGATGCTGACCATCAACCCCTGCCAAGCG 1040
      |||||
Db  291  GGTAACTCTCTGAAGCCGAAAGACTGTATCAACAGATGCTGACCATTAACCCGAGCAAGCG 350
      |||||
QY  1041  CATCACAGCCCATGAGGCGCCTGAAGCACCCGTTGGGCTTGCCACAGCTCCACGGTAGCATC 1100
      |||||
Db  351  CATCACGGCTGACCAAGGCTCTCAAGCACCCGTTGGGCTGTGTCAACGATCCACGGTGGCATC 410
      |||||
QY  1101  CATGATGCACACAGAGAGACTGTGAGAGTCTTGAAAAGTTCAATGCCAGGAGAAAGCT 1160
      |||||
Db  411  CATGATGCATCTGAGGAGACTGTGAGTGTGTGGCAAGTTCAATGCCCGGAGAAACT 470
      |||||
QY  1161  CAAG 1164
      |||
Db  471  GAAG 474

RESULT 13
US-09-918-995-26755
; Sequence 26755, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756

```

```

/ CURRENT FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: US/09/235,076
/ PRIOR FILING DATE: 1999-01-20
/ NUMBER OF SEQ ID NOS: 38054
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO: 26755
/ LENGTH: 536
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(556)
/ OTHER INFORMATION: n = A,T,C or G
US-09-918-995-26755

Query Match          12.7%; Score 282.2; DB 11; Length 556;
Best Local Similarity 93.9%; Pred. No. 1.5e-64;
Matches 293; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY      1276 GAACAAGCCAGAGTTTACTCAACAAGAACGAGATGGAGTCAAGCCCGCAGACGAATAGC 1335
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      171 GCAGCAGCCAGAGTTTACTCAACAAGAACGAGATGGAGTCAAGCCCGCAGACGAATAGC 230

```

```
QY 1336 ACCAAAACAGTGCAGCGCCACACAGCCCAAGAGGAGCGTTCTCTCTGCGCCCTGGAG 1395
Db 231 ACCAAAACAGTGCAGCGCCACACAGCCCAAGAGGAGCGTTCTCTCTGCGCCCTGGAG 290
QY 1396 CTTCAACACACCGTTCATCCATACACCCAGTGGAGCGGATTAAGGAGTCTTCTGACAGTGCC 1455
Db 291 CCTCAACACACCGTTCATCCATACACCCAGTGGAGCGGATTAAGGAGTCTTCTGACAGTGCC 350
QY 1456 AATACACACATAGAGATGAAGACGCTAAAGCCCGGAGCAGGATGATTAAGACACAG 1515
Db 351 AATACACACATAGAGATGAAGACGCTAAAGCCCGGAGCAGGATGATTAAGACACAG 410
QY 1516 GAGCAGCTCATGAGCGCGTCAACAACGCGTACTTTGAGGCTAGCGATTCCTACTTCGAG 1575
Db 411 GAGCGCTCATGAGCGCGTCAACAACGCGTACTTTGAGGCGCTACGGGCGCTACGGGAAATCTGTGAC 470
QY 1576 AACTGTGTGGCC 1587
Db 471 CCAGGGCTGACC 482

RESULT 14
US-09-918-995-26869
; Sequence 26869, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26869
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(476)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-26869
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```
Query Match 11.7%; Score 260.2; DB 11; Length 476;
Best Local Similarity 98.9%; Pred. No. 9.3e-59;
Matches 262; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1276 GAACAAGCCAGAGTTTACTCAACAAGAAAGCAGATGGAGTCAAGCCCGCAGAGCAATAGC 1335
Db 212 GCACAGCCAGAGTTTACTCAACAAGAAAGCAGATGGAGTCAAGCCCGCAGAGCAATAGC 271
QY 1336 ACCAAAACAGTGCAGCGCCACACAGCCCAAGAGGAGCGTTCTCTCTGCGCCCTGGAG 1395
Db 272 ACCAAAACAGTGCAGCGCCACACAGCCCAAGAGGAGCGTTCTCTCTGCGCCCTGGAG 331
QY 1396 CCTCAACACACCGTTCATCCATACACCCAGTGGAGCGGATTAAGGAGTCTTCTGACAGTGCC 1455
Db 332 CCTCAACACACCGTTCATCCATACACCCAGTGGAGCGGATTAAGGAGTCTTCTGACAGTGCC 391
QY 1456 AATACACACATAGAGATGAAGACGCTAAAGCCCGGAGCAGGATGATTAAGACACAG 1515
Db 392 AATACACACATAGAGATGAAGACGCTAAAGCCCGGAGCAGGATGATTAAGACACAG 451
QY 1516 GAGCAGCTCATGAGCGCGTCAACA 1540
Db 452 GAGCAGCTCATGAGCGCGTCAACA 476
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RESULT 15
US-09-918-995-410
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; Sequence 410, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 410
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(461)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-410

Query Match 11.1%; Score 247; DB 11; Length 461;
Best Local Similarity 76.8%; Pred. No. 2.8e-55;
Matches 317; Conservative 0; Mismatches 87; Indels 9; Gaps 1;

QY 903 CTGGGACGAGGACCGACACAGCTGTACCAAGCTGTACCAAGCTGTGCTGCTATGACTGCC 962
Db 40 CGNGAAAAACGGANAGACAAAGCTGTATCATCAGAGATCAAGGCTGGAGCTTATGATTCTC 99
QY 963 GTCCCTGTGAGTGGGACACCGCTCCTCTGAGCCAAACCTCATCAACAGATGCTGAC 1022
Db 100 TTCACCTTAATGGGACACGGTAACTCCTGAAGCCAAAGACTGTATCAACAGATGCTGAC 159
QY 1023 CATCAACCTTGCACAGCGCATCAAGCCCATGAGGCCCTGAAGCACCCTGGTGGTCTGCCA 1082
Db 160 CATAAACCCAGCAAGCGCATCAAGGCTGACGAGCTCTCAAGCACCCTGGTGGTCTGTCA 219
QY 1083 ACGTCCACGGTAGCATCCATGATGACACAGCAGAGACTGTGAGTGTCTGAAAAGTT 1142
Db 220 ACGATCCACGGTGGCATCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 279
QY 1143 CAATGCCAGGAGAAAGCTCAAGGAGGAGCCATCTCAACCCATGCTGGCCACACGGAATTT 1202
Db 280 CAATGCCCGGAGAAAGCTCAAGGAGGAGCCATCTCAAGCCATGCTTGCCTCCAGGAACTT 339
QY 1203 CTCAGTGGGACAGACAGACCCGCTCCGCGCACAAATGTCCACCGCGCTCCGCGCACAC 1262
Db 340 CTCAGTGGGACAGAGAGCTCCGCGCGCGCTCGCTCGCGGAGCGCGCGCGCGCTGGC 399
QY 1263 CATGGGGCTGGTGGACAGCCAGAGTTTACTTACACAGAAACAGATGGAG 1315
Db 400 C-----GGGCAAGCTGCCAAAAGCCCTATTGAAACAAGAAGTCCGATGGC 443

Search completed: October 10, 2003, 08:06:31
Job time : 935 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 10, 2003, 08:08:36 ; Search time 455 Seconds  
(without alignments)  
3061.341 Million cell updates/sec

Title: US-09-820-790B-2

Perfect score: 2715

Sequence: 1 MATVTCRTFTDEYLYEDI.....DGKQNVHFHCGAPVAPLQ 516

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USPfo\_Spool/US09820790/runat\_09102003\_170018\_14752/app\_query.fasta\_1.711  
-DB=N\_Geneseq\_19Jun03 -FWT=fastp -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPEXT=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09820790.acgn.1.1.0 -runat\_09102003\_170018\_14752 -NCPUS=6 -ICPU=3  
-NO\_WMAP -LARGESQUERY -NEG\_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_19Jun03.\*

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.\*  
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.\*  
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25: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2715	100.0	2218	25	AA47686
2	2692	99.2	1727	24	ABZ23378
3	2692	99.2	1727	24	ABZ23379
c	2476.5	91.2	2110	21	AAZ46160
5	2445.5	90.1	1676	21	AAZ46155
6	2241	82.5	1880	24	AAZ26469
7	2230	82.1	1793	24	ABK33805
8	2230	82.1	3015	22	AAK52574
9	2230	82.1	3015	22	AAH99755
10	2225.5	82.0	2061	24	AAZ39316
11	2225.5	82.0	2061	25	ABX10915
12	2222	81.8	3026	22	AAK51590
13	2186.5	80.5	3705	25	ABK63227
14	2177	80.2	5637	24	ABK63630
15	2070	76.2	1500	22	AAU06712
16	2070	76.2	3901	25	ACC46209
17	2054	75.7	2005	23	AAH81013
18	1989	73.3	4078	23	ABK43688
19	1872	69.0	2899	23	ABL17397
20	1872	69.0	3000	23	ABL19677
21	1872	69.0	3468	23	ABL19679
22	1775.5	65.4	1383	25	ABZ77133
23	1568	57.8	1551	21	AAC98200
24	1326	48.8	1107	25	ABZ77134
25	1270.5	46.8	1407	25	ABZ77162
26	1259	46.4	1260	21	AAZ46146
27	1010.5	37.2	867	23	AAH49398
28	978	36.0	17308	23	ABL17396
29	978	36.0	17312	23	ABL19678
30	978	36.0	19648	23	ABL19676
31	854	31.5	1064	23	ABK34399
32	763.5	28.1	1888	22	AAH99231
33	658.5	24.3	854	22	ABH11385
34	628.5	23.1	1736	22	AAH18817
35	618.5	22.8	1694	22	AAC90432
36	618.5	22.8	435	22	AAZ71149
37	618.5	22.8	435	23	ABK43969
38	618	22.8	1578	22	AAZ04775
39	618	22.8	1871	22	AAH25120
40	617.5	22.7	1565	24	ABL60905
41	616.5	22.7	1158	22	AAH25118
42	616.5	22.7	1661	22	AAH18836
43	616.5	22.7	2164	22	AAI60424
44	613.5	22.6	1074	22	AAU06708
45	613.5	22.6	1074	22	AAH25119

# ALIGNMENTS

## RESULT 1

AA47686  
ID AA47686 standard; cDNA; 2218 BP.

XX AA47686;

AC AA47686;

XX 24-FEB-2003 (first entry)

DT Human kinase protein cDNA.

DE Human; calcium/calmodulin-dependent protein kinase; immune response;

XX Human; calcium/calmodulin-dependent protein kinase; immune response;

KW drug screening; carcinoma; inflammation; immune disorder; gene therapy;

XX growth disorder; developmental disorder; chromosome 7; gene; ss.

XX Homo sapiens.

XX Key

XX Location/Qualifiers



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5'UTR      1..261
FT          /*tag= a
FT CDS      262..1812
FT          /*tag= b
FT          /product= "Human kinase protein"
FT 3'UTR    1813..2218
FT          /*tag= c
XX
PN WO200279431-A2.
XX
PD 10-OCT-2002.
XX
PF 01-APR-2002; 2002WO-US09744.
XX
PR 30-MAR-2001; 2001US-0820790.
XX
PA (PEKE ) PE CORP NY.
XX
PA (BEAS/) BEASLEY E M.
XX
PI Shao W, Merkulov GV, Di Francesco V;
XX
DR WPI; 2003-046806/04.
DR P-PSDB; ABE30198.
XX
XX
XX New peptides related to calcium/calmodulin-dependent protein kinase
XX subfamily useful for treating disorders associated with abnormal
XX expression of kinase in fetal brain, testis, lung small cell carcinoma,
XX uterus adenocarcinoma
XX
XX Claim 4; Fig 1A; 86pp; English.
XX
XX The invention relates to new peptides related to calcium/calmodulin-
XX dependent protein kinase subfamily. The peptides are useful in
XX substantial and specific assays related to functional information of the
XX peptide sequences, to raise antibodies or to elicit immune response, as
XX reagents in assays to determine the levels of protein in biological
XX fluids and as markers for tissues where the corresponding protein is
XX expressed. The peptides and antibodies are useful in drug screening
XX assays, tissue typing and pharmacogenomic analysis. They are also useful
XX in treating disorders associated with the absence of, inappropriate or
XX unwanted expression of kinase protein in fetal brain, testis, lung small
XX cell carcinoma or uterus endometrium adenocarcinoma, such as cancer,
XX inflammation, immune disorders or disorders affecting growth and
XX development. The invention is useful as models for the development of
XX human therapeutic targets, aid in the identification of therapeutic
XX proteins and serve as targets for the development of human therapeutic
XX agents that modulate kinase activity in cells and tissues that express
XX the transporter. The host cells are useful in producing a kinase protein
XX or peptide and non-human transgenic animals. The invention is useful in
XX gene therapy. Kinase protein gene is located on chromosome 7. The present
XX sequence is human kinase protein cDNA.
XX
SQ Sequence 2218 BP; 478 A; 727 C; 645 G; 368 T; 0 other;

Alignment Scores:
Pred. No.:      3.68e-242      Length:      2218
Score:          2715.00      Matches:      516
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              25          Gaps:      0

US-09-820-790B-2 (1-516) x AADA7686 (1-2218)
QY      1 MetaLalThrValThrCysThrArgPheThrAspGluThrGlnLeuYrGluAspIle 20
Dd      262 ATGGCCACCACGGTGACCTGCACCCCGCTTCACCGACGAGTACCGAGTCTACAGGATATT 321
QY      21 GlyLysGlyAlaPheSerValValArgCysValLysLeuCysThrGlyHisGluThr 40
Dd      322 GGCACGGGGGGCTTTCTCTGTGTGTCGACGCTGTGTGTCGACGCTGTGTGTCGACGCTGTGT 381
QY      41 AlaAlaLysIleIleAsnThrLysLysLeuSerAlaArgAspHisGlnLysLeuGluArg 60

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Dd      382 GCAGCCAGATCATCAACACCAAGAGAGTGTACCCAGAGATCACCAGAGCTGAGAGA 441
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Dd      442 GAGGCTCGGATCTCGCGCTTCTGAGCATTCACACATCGTGGTCTCCACAGAGATC 501
QY      81 SerGluGluGlyPheHisTyrLeuValPheAspLeuValThrGlyGlyGluLeuPheGlu 100
Dd      502 TCCGAGGAGGGCTTCACCTACCTGCTGTGATCTGGTCACTGGTGGGAGCTCTTTGAA 561
QY      101 AspIleValAlaArgGluThrTyrSerGluAlaAspAlaSerHisCysIleGlnIle 120
Dd      562 GACATTGTGGCGAGAGAGTACTACAGAGAGCTGATGCCAGTCACTGTATCCACAGATC 621
QY      121 LeuGluAlaValLeuHisCysHisGlnMetGlyValValHisArgAspLeuLysProGlu 140
Dd      622 CTGGAGGGCCGTCTTCATTGTCAACCAATGGGGTGTCCACAGAGACCTCAAGCCGGAG 681
QY      141 AsnLeuLeuLeuAlaSerLysCysGlyAlaAlaValLysLeuAlaAspPheGlyLeu 160
Dd      682 AACCTGCTTCTGGCCAGCAAGTCAAGAGGGCTGCAAGTGAAGCTGCGCACTTCGGCTA 741
QY      161 AlaIleGluValGlnGlyAspGlnGlnAlaThrPheGlyPheAlaGlyThrProGlyTyr 180
Dd      742 GCTATCGAGGTGCGAGGGGACCCAGAGCGATGGTGGTTTCGCTGGCACACAGGCTAC 801
QY      181 LeuSerProGluValLeuArgGlyGluAlaTyrGlyLysProValAspIleThrAlaCys 200
Dd      802 CTGTCCCTCAGGTCTCTTCGAAAGAGGCGTATGGCAAGCCTGTGGACATCTGGGCAAT 861
QY      201 GlyValIleLeuTyrIleLeuLeuValGlyTyrProPheThrAspGluAspGlnHis 220
Dd      862 GGGGTGATCTGTACATCTGCTCGTGGCTACCCACCTCTCTGGGAGAGAGACACAC 921
QY      221 LysLeuTyrGlnGlnIleLysAlaGlyAlaTyrAspPheProSerProGluTyrPaspThr 240
Dd      922 AAGCTGTACACAGAGATCAAGGCTGTGCTGCTATGACTTCCCTCCCTGAGTGGGACAC 981
QY      241 ValThrProGluAlaLysAsnLeuIleAsnGlnMetLeuThrIleAsnProAlaLysArg 260
Dd      982 GTCATCTCTGAACCAAAACCTCATCAACAGATGTGACCATCAACCTGACCCCTGCCAAGCC 1041
QY      261 IleThrAlaHisGluAlaLeuLysHisProThrValCysGlnArgSerThrValAlaSer 280
Dd      1042 ATCACAGCCCATGAGCCCTGAAGCACCCGCGGTCTGCAACGCTCCACGAGTACATCC 1101
QY      281 MetMetHisArgGlnGlnThrValGluCysLeuLysLysPheAsnAlaArgArgLysLeu 300
Dd      1102 ATGATGCACACAGAGAGACTGTGGAGTGTCTGAAAAGTTCAATGCCAGGAGAAGCTC 1161
QY      301 LysGlyAlaIleLeuThrThrMetLeuAlaThrArgAsnPheSerValGlyArgGluThr 320
Dd      1162 AAGGGAGCCATCTCCACCATCTGCGCCACACGGAATTTCTCAGTGGGACAGACAC 1221
QY      321 ThrAlaProAlaThrMetSerThrAlaAlaSerGlyThrThrMetGlyLeuValGluGln 340
Dd      1222 ACCGCTCGGCCACAATATGCCACCGGCTTCGGGACACCATCCATGGGCTGGTGGAAACA 1281
QY      341 AlaLysSerLeuLeuAsnLysAlaAspGlyValLysProGlnThrAsnSerThrLys 360
Dd      1282 GCCAAGAGTTTACTTCAACAGAAAGACATGGATGAGCCCGCCAGCCAGCAATAGCACC 1341
QY      361 AsnSerAlaAlaAlaThrSerProLysGlyThrLeuProProAlaAlaLeuGluProGln 380
Dd      1342 ACAGTGCAGCCGCCACCCAGCCCAAGAGGACGCTCTCTCTGCGCCCTCGAGACCTCAA 1401
QY      381 ThrThrValIleHisAsnProValAspGlyIleLysGluSerSerAspSerAlaAsnThr 400
Dd      1402 ACCACCGTCACTCCATAACCCAGTGGAGGGATTAAAGAGTCTTCTGACAGTGCCTAAC 1461
QY      401 ThrIleGluAspGluAspAlaLysAlaArgLysGlnGluIleIleLysThrThrGluGln 420

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Db 1462 ACCATAGAGGTAGACGCTAAGCCGGAAGCAGGAGATCATTAAGACCGAGGAG 1521  
 QY 421 LeuileGluAlaValAsnAsnglyAspPheGluAlaTyrAlaPheTyrPheGluAsnLeu 440  
 Db 1522 CTCATCGAGGCGCTCAACAACGGTGTCTTGAGGCGCTACGCACTTACTTTCAGAACCTG 1581  
 QY 441 LeuAlaLysAsnSerLysProIleHisThrThrIleLeuAsnProHisValIleValle 460  
 Db 1582 CTGGCCAGAGACAGACGAGCGATCCACAGCAACCACTGACCACTGACCACTGACCACT 1641  
 QY 461 GlyGluAspAlaAlaCysIleAlaTyrIleArgLeuThrGlnTyrIleAspGlyGlnGly 480  
 Db 1642 GGAGAGATGCGCGCTCATCGCTTACATCCGGCTCAGCAGTACATTCAGCGGAGGCG 1701  
 QY 481 ArgProArgThrSerGlnSerGluGluThrArgValTrpHisArgArgAspGlyLysTrp 500  
 Db 1702 CGGCCCGGACGAGCCAGCTGTGAGGAGACCGCGTGTGGCCGCGGACGCGAAGTGG 1761  
 QY 501 GlnAsnValHisPheHisCysSerGlyAlaProValAlaProLeuGln 516  
 Db 1762 CAGACGTGCACCTTCCACTGCTCGGGCGGCGCTGTGGCCCGCTGCGCGAG 1809  
 RESULT 2  
 ABZ23378  
 ID ABZ23378 standard; cDNA; 1727 BP.  
 XX  
 AC ABZ23378;  
 XX  
 DT 07-APR-2003 (first entry)  
 XX  
 DE Nucleotide sequence of oestrogen receptor alpha cofactor CF19.  
 KW Human; oestrogen receptor alpha; ER-alpha; CF16; CF17; CF18; CF19; CF40;  
 KW CF41; CF42; CF43; cofactor; osteoporosis; bone disease; reproduction;  
 KW hormonal dysfunction; cancer; cardiovascular disease; atherosclerosis;  
 KW hot flush; mood change; Alzheimer's disease; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 Key Location/Qualifiers  
 FH 4..1632  
 CDS /\*tag= a  
 FT /product= "oestrogen receptor alpha cofactor CF19"  
 FT  
 XX  
 PN W0200270699-A2.  
 XX  
 PD 12-SEP-2002.  
 XX  
 XX 28-FEB-2002; 2002WO-EP02189.  
 XX  
 XX 01-MAR-2001; 2001EP-0105062.  
 XX  
 XX (LION-) LION BIOSCIENCE AG.  
 XX  
 PI Albers M, Ellwanger S, Loeser E, Koegl M;  
 XX  
 XX WPI; 2002-713451/77.  
 DR P-PSDB; ABP70158.  
 XX  
 XX New cofactors of estrogen receptor alpha, designated as CF16, CF17,  
 PT CF18, CF19, CF40, CF41, CF42 and/or CF43, useful for screening of  
 PT compounds for treating osteoporosis, hormonal dysfunctions, cancer or  
 PT cardiovascular diseases -  
 XX  
 XX Claim 1; Page 74; 111pp; English.  
 XX  
 CC The present sequence encodes a cofactor of oestrogen receptor alpha  
 CC (ER-alpha), designated CF19. The specification describes CF16, CF17,  
 CC CF18, CF19, CF40, CF41, CF42, and CF43. The cofactor polypeptides and  
 CC nucleic acid molecules are useful for screening for compounds for  
 CC treating osteoporosis and other bone diseases, failures in reproductive  
 CC functions or hormonal dysfunctions, cancer or cardiovascular diseases  
 CC such as atherosclerosis, and in preventing hot flushes, mood changes

CC and Alzheimer's disease. The CF proteins are also useful for screening  
 CC for ligands of the ER alpha. The nucleic acid sequences are useful for  
 CC making vectors and CF polypeptides, transforming host cells, as research  
 CC tools for developing nucleic acid probes, and for developing analytical  
 CC tools such as antisense oligonucleotides.  
 XX  
 SQ Sequence 1727 BP; 404 A; 531 C; 483 G; 309 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 3,56e-240 Length: 1727  
 Score: 2692.00 Matches: 516  
 Percent Similarity: 95.20% Conservative: 0  
 Best Local Similarity: 95.20% Mismatches: 0  
 Query Match: 99.15% Indels: 26  
 DB: 24 Gaps: 1  
 US-09-820-790b-2 (1-516) x ABZ23378 (1-1727)  
 QY 1 MetalThrThrValThrCysThrArgPheThrAspGluTyrGlnLeuTyrGluAspIle 20  
 Db 4 ATGGCCACACAGGTGACCTGCACCCGCTTCACCCAGGAGTACAGCTCTACAGAGATATT 63  
 QY 21 GlyLysGlyAlaPheSerValValArgArgCysValLysLeuCysThrGlyHisGluTyr 40  
 Db 64 GCGAAGGGGGCTTCTCTGTGTGTCGACGCTGTGTCAAGCTCTGCACCGGCGCATGAGTAT 123  
 QY 41 AlaAlaLysIleIleAsnThrLysLysLeuSerAlaArgAspHisGlnLysLeuGluArg 60  
 Db 124 GCAGCCAAGATCATCACACCAAGAGGTGTCAACCCAGAGATCACCAGAGCTGGAGAGA 183  
 QY 61 GluAlaArgIleCysArgLeuLeuLysHisSerAsnIleValArgLeuHisAspSerIle 80  
 Db 184 GAGGCTCGGATCGCGCCTCTGAGAGCATTCACACATCGTGGCTCCACAGACAGATC 243  
 QY 81 SerGluGluGlyPheHisTyrIleValPheAspLeuValThrGlyGlyGluLeuPheGlu 100  
 Db 244 TCCGAGGAGGGCTTCCACTACCTACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 303  
 QY 101 AspIleValAlaArgGluTyrIleSerGluAlaAspAlaSerHisCysIleGlnIle 120  
 Db 304 GACATTGTGGGAGAGAGTACTACAGCGAGGCTGATGCCAGTCACTGTATCCAGCAGATC 363  
 QY 121 LeuGluAlaValLeuHisCysHisGlnMetGlyValValHisArgAspLeuLysProGlu 140  
 Db 364 CTGGAGGCGCTTCTCCATTGTCAACCAATGGGGTCTCCACAGACACTCAAGCCGAG 423  
 QY 141 AsnLeuLeuAlaSerLysCysLysGlyAlaAlaValLysLeuAlaAspPheGlyLeu 160  
 Db 424 AACCTGCTTCTGGCCAGCAGCAAGTCAAAAGGGGCTGCAAGTGAAGCTGGCACTTCGGCTA 483  
 QY 161 AlaIleGluValGlnGlyAspGlnGlnAlaTrpPheGlyPheAlaGlyThrProGlyTyr 180  
 Db 484 GCTATCGAGGTGCAGGGGGACAGCAGGATGGTTTGGTTTCCCTGGCACACCGGCTAC 543  
 QY 181 LeuSerProGluValLeuArgLysGluAlaTyrGlyLysProValAspIleTrpAlaCys 200  
 Db 544 CTGTCCCTCGAGTCTTCTGCAAGAGGCGTATGGCAAGCCTGTGGACATCTGGGCGATGT 603  
 QY 201 GlyValIleLeuTyrIleLeuValGlyTyrProPheThrAspGluAspIleHis 220  
 Db 604 GGGGTGATCTGTGTACATCTGCTGGGGCTACCCACCCCTTCGGGACGAGACGACGAC 663  
 QY 221 LysLeuTyrGlnGlnIleLysAlaGlyAlaTyrAspPheProSerProGluTrpAspThr 240  
 Db 664 AAGCTGTACACAGACATCAAGGCTGTGTGCTATGACTTCCGCTCCCTGAGTGGGACACC 723  
 QY 241 ValThrProGluAlaLysAsnLeuIleAsnGlnMetLeuThrIleAsnProAlaLysArg 260  
 Db 724 GTCACTCTCGAAGCAAAAACCTCATCAACAGATGTGACCATCAACCTGCCAAGCGC 783  
 QY 261 IleThrAlaHisGluAlaLeuLysHisProTrpValCysGlnArgSerThrValAlaSer 280  
 Db 784 ATCAGACCCCATGAGGCGCTGAAGACACCGGTGGGTCTGCAACAGCTCCACGCTAGCATCC 843

QY 281 MetMetHisArgGlnGluThrValGluCysLeuLysPheAsnAlaArgArgLysLeu 300  
 Db 844 ATGATGACACAGAGAGAGACTGTGAGTGTCTGAAAGGTCAATGCCAGAGAGAGCTC 903  
 QY 301 LysGlyAlaLeuThrThrMetLeuAlaThrArgAsnPheSerValGlyArgGlnThr 320  
 Db 904 RAGGAGCCATCTCACCACCATGTGGCCACAGGAATTTCTCAGTGGCAGACAGACC 963  
 QY 321 ThrAlaProAlaThrMetSerThrAlaAlaSerGlyThrThrMetGlyLeuValGluGln 340  
 Db 964 ACCGCTCGGCCCAATGTCACCGCGCTCCGGCACCACCATGGGTGGTGGACAA 1023  
 QY 341 AlaLysSerLeuLeuAsnLysLysAlaAspGlyValLysProGlnThrAsnSerThrLys 360  
 Db 1024 GCCAAGAGTTTACTCAACAAAGACAGATGGAGTCAAGCCACAGCAATAGCAGAA 1083  
 QY 361 AsnSerAlaAlaThrSerProLysGlyThrLeuProAlaAlaLeuGluProGln 380  
 Db 1084 AACAGTGCAGCGCCACCAAGCCCAAGAGGACGCTTCTCCTCGCGCCTGGAGCTCAA 1143  
 QY 381 ThrThrValIleHisAsnProValAspGlyIleLysGluSerSerAspSerAlaAsnThr 400  
 Db 1144 ACCACGCTCATCAATACCATGTCGACGGGATTAAGAGTCTCTGACAGTGCCTAATCC 1203  
 QY 401 ThrIleGluAspGluAspAlaLysAlaArgLysGlnIleIleLysThrThrGluGln 420  
 Db 1204 ACCATAGAGTGAAGACGCTAAAGCCCGGAAGCAGGAGATCATTAAGACCCAGGACAG 1263  
 QY 421 LeuIleGluAlaValAsnAsnGlyAspPheGluAlaTyrAla----- 434  
 Db 1264 CTCATCGAGCGCTCAACACCGTGACCTTTGAGCGCTTACGCGAAATCTGTGCCACAGG 1323  
 QY 434 ----- 434  
 Db 1324 CTGACCTGTTTGAGCTGAAGCACTGGGCAACCTGTTGAGGGGATGCTTCCACAGA 1383  
 QY 435 PheTyrPheGluAsnLeuLeuAlaLysAsnSerLysProIleHisThrIleLeuAsn 454  
 Db 1384 TTCTACTTCGAGAACCTGTGCGCAAGACAGCAGACCGATCCACACGACCATCTCTGAAC 1443  
 QY 455 ProHisValHisValIleGlyGluAspAlaAlaCysIleAlaTyrIleArgLeuThrGln 474  
 Db 1444 CCACAGCTGACGTCATTGGAGAGATGCCCGCTGCATCGCTTACATCCGCTCAGCAG 1503  
 QY 475 TyrIleAspGlyGlnGlyArgProArgThrSerGlnSerGlnGluThrArgValTrpHis 494  
 Db 1504 TACATTGACGGCAGCGCGCGCGCCGACACCGACGCTGAGAGAGCCGCGGTGGCAC 1563  
 QY 495 ArgArgAspGlyLysTrpGlnAsnValHisPheHisCysSerGlyAlaProValAlaPro 514  
 Db 1564 CCGCCGACGCGAGTGGCAGAACGTGCACCTCCACTTCCACTGCTCGGGCGCGCTGTGGCCCG 1623  
 QY 515 LeuGln 516  
 Db 1624 CTGCAG 1629  
 RESULT 3  
 ABZ23379/c  
 ID ABZ23379 standard; cDNA; 1727 BP.  
 XX AC ABZ23379;  
 XX AC  
 XX AC  
 XX 07-APR-2003 (first entry)  
 XX DE Reverse complement of oestrogen receptor alpha cofactor CF19 cDNA.  
 XX DE Human; oestrogen receptor alpha; ER-alpha; CF16; CF17; CF18; CF19; CF40;  
 KW CF41; CF42; CF43; cofactor; osteoporosis; bone disease; reproduction;  
 KW hormonal dysfunction; cancer; cardiovascular disease; atherosclerosis;  
 KW hot flush; mood change; Alzheimer's disease; ss.  
 XX Homo sapiens.  
 OS

XX PN WO200270699-A2.  
 XX PD 12-SEP-2002.  
 XX PF 28-FEB-2002; 2002WO-EP02189.  
 XX PR 01-MAR-2001; 2001EP-0105062.  
 XX PA (LION-) LION BIOSCIENCE AG.  
 XX PI Albers M, Ellwanger S, Loeser E, Koegl M;  
 XX WPI; 2002-713451/77.  
 XX DR New cofactors of estrogen receptor alpha, designated as CF16, CF17,  
 XX CF18, CF19, CF40, CF41, CF42 and/or CF43, useful for screening of  
 XX PT compounds for treating osteoporosis, hormonal dysfunctions, cancer or  
 XX PT cardiovascular diseases -  
 XX PS Claim 1; Page 75-76; 11pp; English.  
 XX CC The present sequence represents the reverse complement of cDNA encoding  
 XX CC a cofactor of oestrogen receptor alpha (ER-alpha), designated CF19. The  
 XX CC specification describes CF16, CF17, CF18, CF19, CF40, CF41, CF42, and  
 XX CC CF43. The cofactor polypeptides and nucleic acid molecules are useful  
 XX CC for screening for compounds for treating osteoporosis and other bone  
 XX CC diseases, failures in reproductive functions or hormonal dysfunctions,  
 XX CC cancer or cardiovascular diseases such as atherosclerosis, and in  
 XX CC preventing hot flushes, mood changes and Alzheimer's disease. The CF  
 XX CC proteins are also useful for screening for ligands of the ER alpha. The  
 XX CC nucleic acid sequences are useful for making vectors and CF polypeptides,  
 XX CC transforming host cells, as research tools for developing nucleic acid  
 XX CC probes, and for developing analytical tools such as antisense  
 XX CC oligonucleotides.  
 XX SQ Sequence 1727 BP; 309 A; 483 C; 531 G; 404 T; 0 other;

Alignment Scores:  
 Pred. No.: 3.56e-240 Length: 1727  
 Score: 2692.00 Matches: 516  
 Percent Similarity: 95.20% Conservative: 0  
 Best Local Similarity: 95.20% Mismatches: 0  
 Query Match: 99.15% Indels: 26  
 DB: 24 Gaps: 1

US-09-820-790B-2 (1-516) x ABZ23379 (1-1727)

QY 1 MetAlaThrThrValThrCysThrArgPheThrAspGluTyrGlnLeuTyrGluAspIle 20  
 Db 1724 ATGCCACACAGGTGACCTGACCCCGCTTCACGACGAGTACCAGCTCTACGAGGATAT 1665  
 QY 21 GlyLysGlyAlaPheSerValValArgCysValLysLeuCysThrGlyHisGluTyr 40  
 Db 1664 GGCAGGGGGCTTCTCTGTGTCCGACGCTGTCAAGCTCTGCACGCCCATAGATAT 1605  
 QY 41 AlaAlaLysIleIleAsnThrLysLysLeuSerAlaArgAspHisGlnLysLeuGluArg 60  
 Db 1604 GCAGCCAAAGATCATCAACACCAAGAGCTGTCCAGCAGAGATCACAGAGCTGGAGAGA 1545  
 QY 61 GluAlaArgIleCysArgLeuLeuLysHisSerAsnIleValArgLeuHisAspSerIle 80  
 Db 1544 GAGCTCGGATCTGCGCGCTTCTGACCATTCACATCGCTGCGCTCCACGACACATC 1485  
 QY 81 SerGluGluGlyPheHisTyrLeuValPheAspLeuValThrGlyGlyGluLeuPheGlu 100  
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 QY 101 AspIleValAlaArgGluTyrTyrSerGluAlaAspAlaSerHisCysIleGlnGlnIle 120  
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 QY 121 LeuGluAlaValLeuHisCysHisGlnMetGlyValValHisArgAspLeuLysProGlu 140

|||||  
1364 CTGGAGCGCGTCTCCATTGTCACAAATGGGGTCTCCACAGACACTCAAGCGGAG 1305  
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141 AsnLeuLeuLeuAlaSerLysCysLysGlyAlaAlaValLysLeuAlaAspPheGlyLeu 160  
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161 AlaIleGluValGlnGlyAspGlnAlaTrpPheGlyPheAlaGlyThrProGlyTyr 180  
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1244 GCTATCGAGGTGCAGGGGGACAGCAGCATGGTTGGTTCTGGCACACAGGCTAC 1185  
QY |||||  
181 LeuSerProGluValLeuLeuGlyLysGluAlaTrpGlyLysProValAspIleTrpAlaCys 200  
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201 GlyValIleLeuTyrIleLeuLeuValGlyTyrProPheTrpAspGluAspGlnHis 220  
Db |||||  
1124 GGGGTGATCTGTACATCCCTGCTGGTGGCTACCCACCCTCTGGGACGAGGACACGAC 1065  
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361 AsnSerAlaAlaAlaThrSerProLysGlyThrLeuProAlaAlaLeuGluProGln 380  
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381 ThrThrValIleHisAsnProValAspGlyIleLysGluSerSerAspSerAlaAsnThr 400  
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QY |||||  
401 ThrIleGluAspGluAspAlaLysAlaArgLysGlnGluIleLysThrThrGluGln 420  
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524 ACCATAGAGATGAAGAGCTTAAGCCCGGAAGCAGGAGATCATTAAGACACGAGGAG 465  
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421 LeuIleGluAlaValAsnAsnGlyAspPheGluAlaTyrAla----- 434  
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464 CTATCGAGCGCTCAACAGGTGACTTTGAGGCTACGGGAAATCTGTGACCCAGGG 405  
QY |||||  
434 ----- 434  
Db |||||  
404 CTGACCTCGTTTGACCTGAAGCACTGGGCAACCTGGTTGAAGGATGGACTTCCACAGA 345  
QY |||||  
435 PheTyrPheGluAsnLeuAlaLysAsnSerLysProIleHisThrThrIleLeuAsn 454  
Db |||||  
344 TTCATCTGAGAACTCTGCGCAAGACAGACGCGGATCCACAGACATCTGTGAC 285  
QY |||||  
455 ProHisValHisValIleGlyLysAlaAlaCysIleAlaTyrIleArgLeuThrGln 474  
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Db 284 CCACACCTGCACCTCATTTGGAGAGGATCGCGCTGCATCGCTTACATCCGGCTCAGCGAG 225  
QY 475 TyrIleAspGlyGlnGlyArgProArgThrSerGlnSerGluGluThrArgValTrpHis 494  
|||||  
Db 224 TACATTCACGGGAGGGCGGCGCCGCCACGACCATCTCTGAGGAGACCGCGTGTGGCAC 165  
QY 495 ArgArgAspGlyLysTrpGlnAsnValHisPheHisCysSerGlyAlaProValAlaPro 514  
Db 164 CGCGCGACGCGCAAGTGGCAGAACGTGCATCTCCACTGCTCGGCGCGCTGTGGCCCG 105  
QY 515 LeuGln 516  
|||||  
Db 104 CTGCGAG 99  
RESULT 4  
AAZ46160  
ID AAZ46160 standard; cDNA; 2110 BP.  
XX AC AAZ46160;  
AC AAZ46160;  
XX 16-MAY-2000 (first entry)  
DT cDNA sequence encoding a human phosphorylation effector PHS-23.  
DE Human; phosphorylation effector; PHS; proliferative disorder;  
XX Human; phosphorylation effector; PHS; proliferative disorder;  
KW immune disorder; neuronal disorder; ss.  
KW Homo sapiens.  
OS  
XX  
FH Key Location/Qualifiers  
FT CDS 25..1950  
FT FT /\*tag= a  
FT FT /product= "phosphorylation effector"  
XX  
PN W0200006728-A2.  
XX 10-FEB-2000.  
XX 28-JUL-1999; 99WO-US17132.  
XX 28-JUL-1998; 98US-0123494.  
PR 14-SEP-1998; 98US-0152814.  
PR 14-OCT-1998; 98US-0173482.  
PR 03-NOV-1998; 98US-0106889.  
PR 19-NOV-1998; 98US-0109093.  
PR 22-DEC-1998; 98US-0113796.  
PR 12-JAN-1999; 99US-0173482.  
PR 12-JAN-1999; 99US-0229005.  
XX (INCY-) INCYTE PHARM INC.  
XX Hillman JL, Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR;  
PI Patterson C, Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;  
PI Reddy R, Lu DAM, Shih LI;  
XX WPI; 2000-183125/16.  
DR P-PSDB; AA168791.  
DR  
XX New human phosphorylation effectors useful for the diagnosis, treatment  
PT and prevention of proliferative, immune and neuronal disorders -  
XX  
XX Claim 9; Page 136; 142pp; English.  
XX  
CC AAZ46138-246168 encode human phosphorylation effectors (PHSP),  
CC designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not given  
CC in the specification). The sequences were isolated from cDNA libraries  
CC prepared from various human tissues. The PHSP proteins are useful for  
CC the diagnosis, treatment and prevention of proliferative disorders,  
CC immune disorders and neuronal disorders. The PHSP proteins form  
CC pharmaceutical compositions which useful for treating or preventing  
CC disorders associated with decreased PHSP expression/activity. PHSP  
CC antagonists are useful for treating or preventing disorders associated  
CC with increased PHSP expression/activity.

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xx
SQ Sequence 2110 BP: 466 A; 688 C; 577 G; 379 T; 0 other;

Alignment Scores:
Pred. No.: 4,95e-220 Length: 2110
Score: 2476.50 Matches: 491
Percent Similarity: 73.72% Conservative: 0
Best Local Similarity: 73.72% Mismatches: 0
Query Match: 91.22% Indels: 175
DB: 21 Gaps: 3

US-09-820-790b-2 (1-516) x AN246160 (1-2110)

QY 1 MetAlaThrThrValThrCysThrArgPheThrAspGluTyrGlnLeuTyrGluAspIle 20
DB 25 ATGGCCACCACGGTGACCTGACCGCTTCACGACGAGTACACCTCTACGAGGATATT 84
QY 21 GlyTyrGlyAlaPheSerValValArgCysValLysLeuCysThrGlyHisGluTyr 40
DB 85 GGCAGGGGGCTTCTCTGTGTCGACGCTGTCTCAAGCTCTGCACCGGCCATGAGTAT 144
QY 41 AlaAlaLysIleIleAsnThrLysLysLeuSerAlaArgAspHisGlnLysLeuGluArg 60
DB 145 GCAGCCAGATCATCACACCAAGAGCTGTACGCCAGAGATCACCAAGAGTGGAGAGA 204
QY 61 GluAlaArgIleCysArgLeuLeuLysHisSerAsnIleValArgLeuHisAspSerIle 80
DB 205 GAGGCTCGGATCTGGCGCTTCTGAAGCATTCACATCCATCGTGCCTCCACGACGATC 264
QY 81 SerGluGluGlyPheHisTyrLysLeuValPheAspLeuValThrGlyGlyLeuPheGlu 100
DB 265 TCCGAGGAGGGCTTCACCTACCTGCTGTGATCTGTCTGCTGCTGCTGCTGCTGCTG 324
QY 101 AspIleValAlaArgGluTyrTyrSerGluAlaAspAlaSerHisCysIleGlnIle 120
DB 325 GACATTTGGCGAGAGAGTACTACAGCGAGCTGTGTCGACCTGTATCCACGATC 384
QY 121 LeuGluAlaValLeuHisCysHisGlnMetGlyValValHisArgAspLeuLysProGlu 140
DB 385 CTGGAGGCCGTTCTCCATTTGTCACCAATGGGGTGTCCACAGAGACCTCAAGCGGAG 444
QY 141 AsnLeuLeuLeuAlaSerLysCysLysGlyAlaAlaValLysLeuAlaAspPheGlyLeu 160
DB 445 AACCTGCTTCTGCCAGCAAGTGCACAAAGGGGCTGCATGAAGCTGGCAGCTGGCCCTA 504
QY 161 AlaIleGluValGlnGlyAspGlnAlaTrpPheGlyPheAlaGlyThrProGlyTyr 180
DB 505 GCTATCGAGGTGCAGGGGACACGACGATGGTTGGTTTGGCTGGGCACACAGGCTAC 564
QY 181 LeuSerProGluValLeuArgLysGluAlaTyrGlyLysProValAspIleTrpAlaCys 200
DB 565 CTGTCCCTTGAGTCTCTCGCAAGAGCGGTATGGCAAGCCTGTGGACATCTGGGCATGT 624
QY 201 GlyValIleLeuTyrIleLeuLeuValGlyTyrProPheTrpAspGluAspGlnHis 220
DB 625 GGGGTGATCTGTACATCTGCTGTGGCTACCCACCTTCTGGAGACGAGCAGGCAC 684
QY 221 LysLeuTyrGlnGlnIleLysAlaGlyAlaTyrAspPheProSerProGluTrpAspThr 240
DB 685 AAGGTGTACAGAGATCAAGGCTGGTGCCTATGACTTCCCGTCCCTCTGAGTGGGACAC 744
QY 241 ValThrProGluAlaLysAsnLeuIleAsnGlnMetLeuThrIleAsnProAlaLysArg 260
DB 745 GTCACTCTGAACCCAAAACCTCATCACCCAGATGTCACCATCAACCTTCCCAAGCGC 804
QY 261 IleThrAlaHisGluAlaLeuLysHisProTrpValCysGlnArgSerThrValAlaSer 280
DB 805 ATCACAGCCCATGAGGCCCTGAAGCACCCTGGGTCTGCCACGCTCCACGAGCATCC 864
QY 281 MetMetHisArgGlnGluThrValGlnCysLeuLysLysPheAsnAlaArgLysLeu 300
DB 865 ATGATGCACAGACAGAGACTGTGGAGTGTCTGAAAAAGTTCAATGCCAGGAGAAAGCTC 924

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QY 301 LysGlyAlaIleLeuThrThrMetLeuAlaThrArgAsnPheSerValGlyArgGlnThr 320
DB 925 AAGGAGCCATCTCACCACCATCTGGCCACACGGAATTCTCA----- 969
QY 321 ThrAlaProAlaThrMetSerThrAlaAlaSerGlyThrThrMetGlyLeuValGluGln 340
DB 969 ----- 969
QY 341 AlaLysSerLeuLeuAsnLysLysAlaAspGlyValLysProGlnThrAsnSerThrLys 360
DB 970 GCCAAGAGTTTACTCACCAAGAAAGCAGTAGTGAAGTCAAGCCCAAGCAAGCAATCCACAAA 1029
QY 361 AsnSerAlaAlaThrSerProLysGlyThrLeuProAlaAlaLeuGluProGln 380
DB 1030 AACAGTGCAGCCGCCACAGCCCAAGGAGCGCTTCTCTGCGCCCTGGAGCCTCAA 1089
QY 381 ThrThrValIleHisAsnProValAspGlyIleLysGluSerSerAspSerAlaAsnThr 400
DB 1090 ACCACGCTCATCATCAACCCAGTGGACGGANTAAAGAGTCTTCTGACAGTGCCATAAC 1149
QY 401 ThrIleGluAspGluAspAlaLysAla----- 409
DB 1150 ACCATAGAGATGAAGACGCTAAAGCCCCCAGGGTCCCGACATCTCTGAGCTCAGTGAGG 1209
QY 409 ----- 409
DB 1210 AGGGCTCGGGAGCCCAAGAGCCGAGGGGCCCTGCTGCCCTGCCCATCTCCGGCTCCCTTT 1269
QY 409 ----- 409
DB 1270 GGCCCTCCGACGCTCCATCCGCCAGGATCTCTGACATCTCTGAACCTCTGTGAGAGGGGT 1329
QY 409 ----- 409
DB 1330 TCAGGAACCCAGAGACCGAGGGGCCCTCTCAGGGGGGCCCGCCCTGCTGTGTCTCG 1389
QY 409 ----- 409
DB 1390 GCTCTCTAGGCCCTCTGCTCTCCCGTCCCGCAGGATCTCTGACATCTCTGAACCTCTG 1449
QY 409 ----- 409
DB 1450 AGGAGGGGTCAAGGACCCCAAGAGCCAGAGGCCCTCCGCCAGTGGGGCCCCCGCCCTGC 1509
QY 410 -----ArgLysGlnGluIleLys 416
DB 1510 CCATCTCCGACTATCCCTGGCCCCCTGCCACCCCATCCCGAGCAGGAGATCATTAAG 1569
QY 417 ThrThrGluGlnLeuIleGluAlaValAsnAsnGlyAspPheGluAlaTyrAla----- 434
DB 1570 ACCACGAGCAGCTCATCGAGCGCGTCAACAGCGTGAATTTGAGGCTACGGGCAAAATC 1629
QY 434 ----- 434
DB 1630 TGTGACCCAGGCTGACCTCGCTTTGAGCCTGAAGACATGGGCAACCTGTTGAGGGATG 1689
QY 435 -----PheTyrPheGluAsnLeuLeuAlaLysAsnSerLysProIleHisThr 450
DB 1690 GACTTCCACAGATTTCTACTTCGAGAACCTGCTGGCCAAAGACAAAGCAAGCAATCCACAG 1749
QY 451 ThrIleLeuAsnProHisValHisValIleGlyGluAspAlaAlaCysIleAlaTyrIle 470
DB 1750 ACCATCTGAACCCCAAGCTGACGTATTGGAGAGGATGCCGCTGCATCGCTTACATC 1809
QY 471 ArgLeuThrGlnTyrIleAspGlyGlnArgProArgThrSerGlnSerGluGluThr 490
DB 1810 CGSCTCACGCACTACATTGACGGCAGGGCCGGCCCCCAGCCACCTGAGTCTGAGGAGACC 1869
QY 491 ArgValTrpHisArgAspGlyLysTrpGlnAsnValHisPheHisCysSerGlyAla 510
DB 1870 CGCGTGTGGCAGCGCGGAGCGCAGTGGCAGAAATGTGCACTTCCACTTCCACTGCTCGGCGCG 1929
QY 511 ProValAlaProLeuGln 516

```

Db 1930 CCTGTGGCCCGCTGCAG 1947  
|||||

RESULT 5  
AAZ46155  
ID AAZ46155 standard; cDNA; 1676 BP.

XX AAZ46155;  
XX 16-MAY-2000 (first entry)

XX cDNA sequence encoding a human phosphorylation effector PHSP-18.

XX Human; phosphorylation effector; PHSP; proliferative disorder;  
KW immune disorder; neuronal disorder; ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH 25.1535  
FT CDS  
FT /\*tag= a  
FT /product= "phosphorylation effector"

XX WO200006728-A2.

PN 10-FEB-2000.

XX 28-JUL-1999; 99WO-US17132.

XX 28-JUL-1998; 98US-0123494.

PR 14-SEP-1998; 98US-0152814.

PR 14-OCT-1998; 98US-0173482.

PR 03-NOV-1998; 98US-0106889.

PR 19-NOV-1998; 98US-0108093.

PR 22-DEC-1998; 98US-0133796.

PR 12-JAN-1999; 99US-0173482.

PR 12-JAN-1999; 99US-0229005.

XX (INCY-) INCYTE PHARM INC.

XX Hillman JL, Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR;  
PI Patterson C, Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;  
PI Reddy R, Lu DAM, Shih LL;

XX WPI; 2000-183125/16.

DR P-PSDB; AAY68786.

XX New human phosphorylation effectors useful for the diagnosis, treatment  
PT and prevention of proliferative, immune and neuronal disorders -  
XX P-PSDB; AAY68786.

XX Claim 9; Page 132; 142pp; English.

XX AAZ46138-Z46168 encode human phosphorylation effectors (PHSP),  
CC designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not given  
CC in the specification). The sequences were isolated from cDNA libraries  
CC prepared from various human tissues. The PHSP proteins are useful for  
CC the diagnosis, treatment and prevention of proliferative disorders,  
CC immune disorders and neuronal disorders. The PHSP proteins form  
CC pharmaceutical compositions which useful for treating or preventing  
CC disorders associated with decreased PHSP expression/activity. PHSP  
CC antagonists are useful for treating or preventing disorders associated  
CC with increased PHSP expression/activity.

XX Sequence 1676 BP; 385 A; 520 C; 466 G; 305 T; 0 other;

Alignment Scores:  
Pred. No.: 2,73e-217 Length: 1676  
Score: 2445.50 Matches: 475  
Percent Similarity: 87.64% Conservative: 0  
Best Local Similarity: 87.64% Mismatches: 2  
Query Match: 90.07% Indels: 65  
DB: 21 Gaps: 3

US-09-820-790B-2 (1-516) x AAZ46155 (1-1676)

QY 1 MetAlaThrThrValThrCysThrArgPheThrAspGluTyrGlnLeuTyrGluAspIle 20  
DB 25 ATGGCCACCCAGGTGACCTGCACCGCTTACCCAGGAGTACAGCTCTACGAGATATT 84  
QY 21 GLYSGlyAlaPheSerValValArgCysValLysLeuCysThrGlyHisGluTyr 40  
DB 85 GCGAAGGGGGCTTCTCTGTGGTCCGAGCTGTCAAGCTGTGACCGGCGCATGATAT 144  
QY 41 AlaAlaLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 60  
DB 145 GCAGCCAGATCATCAACACCAAGAGCTGCACCCAGAGATCACCAAGACTGGAGAGA 204  
QY 61 GluAlaArgLecysArgLeuLeuLysHisSerAsnLysValValArgLysHisAspSerIle 80  
DB 205 GAGGCTGGATCTCCCGCTTCTGAAGCATTCCTCAACATGCTGCTCCAGAGCATC 264  
QY 81 SerGluGluGlyPheHisTyrLeuValPheAspLeuValThrGlyGlyGluLeuPheGlu 100  
DB 265 TCCGAGGAGGCTTCCACTACCTGGTCTTCGATCTGGTCTACCTGGTGGGAGCTCTTTGAA 324  
QY 101 AspIleValAlaArgGluTyrTyrSerGluAlaAspAlaSerHisCysIleLeuIle 120  
DB 325 GACATTGTGGGAGAGTACTACAGCGAGGCTGATGCCAGTCACTGTATCCAGCATC 384  
QY 121 LeuGluAlaValLeuHisCysHisGlnMetGlyValValHisArgAspLeuLysProGlu 140  
DB 385 CTGGAGGCGCTTCTCCATTGTACCAAAATGGGGTCTCCAGAGACTCAAGCCGGAG 444  
QY 141 AsnLeuLeuLeuAlaSerLysCysLysGlyAlaAlaValLysLeuAlaAspPheGlyLeu 160  
DB 445 AACCTGCTTCTGGCCAGCAGAGTCAAGAGGCTGCAGTGAAGCTGGCAGACTTGGGCTA 504  
QY 161 AlaIleGluValGlnGlyAspGlnGlnAlaThrPheCysIleAlaGlyThrProGlyTyr 180  
DB 505 GCTATCGAGGTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 564  
QY 181 LeuSerProGluValLeuArgLysGluAlaTyrGlyLysProValAspIleTrpAlaCys 200  
DB 565 CTGTCTCTCTGAGTCTCTCGCAAGAGGCTGACGCAAGCCGCTGGACATCTGGGATGT 624  
QY 201 GlyValIleLeuTyrIleLeuLeuValGlyTyrProPheThrAspGluAspGlnHis 220  
DB 625 GGGGTGATCTCTGATACATCTGCTGCTGGGCTACCAACCTCTCTGGGAGGAGGAGCAG 684  
QY 221 LysLeuTyrGlnGlnIleLysAlaGlyAlaTyrAspPheProSerProGluTyrAspThr 240  
DB 685 AAGCTGTACACAGCAGATCAGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 744  
QY 241 ValThrProGluAlaLysAsnLeuLeuAsnGlnMetLeuThrIleAsnProAlaLysArg 260  
DB 745 GTCACTCTCTGAGGCAAAACCTCATCAACAGATGCTGACCATCAACCTGCCAAGCGC 804  
QY 261 IleThrAlaHisGluAlaLeuLysHisProThrValCysGlnArgSerThrValAlaSer 280  
DB 805 ATCAAGCCCATGAGGCGCTTCAAGCAGCCGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 864  
QY 281 MetMetHisArgGlnGlnThrValGluCysLeuLysLysPheAsnAlaArgArgLysLeu 300  
DB 865 ATGATGTCAACAGCAGAGACTGTGGAGTGTCTGAAAAGTTCAATGCCAGGAGAAAGCTC 924  
QY 301 LysGlyValIleLeuThrThrMetLeuAlaThrArgAsnPheSerValGlyArgGlnThr 320  
DB 925 AAGGAGGCGCATCTCCACCATGCTGGCCACACGGAATTTCTCAGCA----- 972  
QY 321 ThrAlaProAlaThrMetSerThrAlaAlaSerGlyThrThrMetGlyLeuValGln 340  
DB 972 ----- 972  
QY 341 AlaLysSerLeuLeuAsnLysLysAlaAspGlyValLysProGlnThrAsnSerThrLys 360  
DB 973 GCCAAGAGTTTACTCAACAAAGAAAGCAGATGGATGAGTCAAGCCCATACGAAATAGACCAAA 1032

QY 361 AsnSerAlaAlaThrSerProLysGlyThrLeuProPrcAlaAlaLeuGluProGln 380  
 |||||  
 Db 1033 AACAGTGCAGCGCCACAGCCCAAGAGGACGCTCTCTCGCGCCCTG----- 1083  
 QY 381 ThrThrValIleHisAsnProValAspGlyIleLysGluSerSerAspSerAlaAsnThr 400  
 |||||  
 Db 1084 -----GAGTCTTCTGACAGTGCCATAAC 1107  
 QY 401 ThrIleGluAspGluAspAlaAlaAlaArgLysGlnGluIleLysThrThrGluGln 420  
 |||||  
 Db 1108 ACATAGAGGATGAGAGCGCTAAAGCCGGAAGCAGGAGCATTAAGACCGAGGAGCAG 1167  
 QY 421 LeuIleGluAlaValAsnAsnGlyAspPheGluAlaTyraAla----- 434  
 Db 1168 CTCATCGAGCGCGTCAACAACGGTGACTTTGAGGCGCTACGGGAAATCTGTGACCCAGG 1227  
 QY 434 ----- 434  
 Db 1228 CTGACCTCGTTTGACCTGAAGCACTGGGCAACCTGGTTGAAGGGATGAGTCTCCACAGA 1287  
 QY 435 PheTyrrPheGluAsnLeuAlaLysAsnSerLysProIleHisThrThrIleLeuAsn 454  
 |||||  
 Db 1288 TTTCTACTTCGAGAACTCTGCGCCAGAGACAGCAGCGGATCCACAGACCATCTTGAC 1347  
 QY 455 ProHisValHisValIleGlyGluAspAlaAlaCysIleAlaTyrrIleArgLeuThrGln 474  
 |||||  
 Db 1348 CCACAGTGCAGCTCATTTGGAGAGGATCGCGCTGATCGCTTACATCCGGCTCAGCGCAG 1407  
 QY 475 TyrrIleAspGlyGlnGlyArgProArgThrSerGlnSerGluGluThrArgValThrPHis 494  
 |||||  
 Db 1408 TACATTCAGGGCAGGGCGGCGCCGACGAGCAGTGTGAGAGAGCCCGCTGTGGCAG 1467  
 QY 495 ArgArgAspGlyLysTrpGlnAsnValHisPheHisCysSerGlyValaProValAlaPro 514  
 |||||  
 Db 1468 CGCGCGAGGCACTGCGCAGAGCTGCTCCACTTCCACTGCTCGGGCGGCTGTGGCCCG 1527  
 QY 515 LeuGln 516  
 |||||  
 Db 1528 CTGCAG 1533  
 RESULT 6  
 ID AAD26469 standard; cDNA; 1880 BP.  
 AC AAD26469;  
 DT 26-MAR-2002 (first entry)  
 DE Human kinase PKIN-22 cDNA.  
 KW Human; kinase; PKIN-22; cancer; leukaemia; adenocarcinoma; osteoporosis;  
 KW immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;  
 KW Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;  
 KW allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;  
 KW autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis;  
 KW Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;  
 KW rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;  
 KW hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;  
 KW cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;  
 KW congestive heart failure; ischaemic heart disease; lung tumour; gout;  
 KW fatty liver; Niemann-Pick's disease; gene therapy; chromosome 10; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 CDS 83..1849  
 FT /tag= a  
 FT /product= "Human PKIN-22 protein"  
 XX WO200196547-A2.  
 XX 20-DEC-2001.

XX 14-JUN-2001; 2001WO-US19444.  
 XX  
 PR 15-JUN-2000; 2000US-212073P.  
 PR 23-JUN-2000; 2000US-213467P.  
 PR 30-JUN-2000; 2000US-215651P.  
 PR 07-JUL-2000; 2000US-216605P.  
 PR 13-JUL-2000; 2000US-218372P.  
 PR 25-AUG-2000; 2000US-228056P.  
 XX (INCY-) INCYTE GENOMICS INC.  
 XX  
 PI Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y;  
 PI Gandhi AR, Tribouley CM, Wallia NK, Yao MG, Lu DAM, Greenwald SR;  
 PI Rankumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT;  
 PI Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;  
 PI Lo IP, Khan F, Riccapon SA, Azimzal Y, Policky JL, Ding L;  
 PI Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;  
 XX  
 DR WPI; 2002-090207/12.  
 DR P-PSDB; AAE16276.  
 XX  
 PT New polypeptides, useful for diagnosing, treating or preventing  
 PT disorders of growth and development, cardiovascular and lipid, and  
 PT diseases such as cancer, comprise human kinase polypeptides -  
 PS  
 PS Claim 5; Page 193; 197pp; English.  
 XX  
 CC The invention relates to human kinase PKIN proteins and their  
 CC corresponding cDNAs. A composition containing PKIN agonist is useful for  
 CC treating a disease or condition associated with decreased expression of  
 CC PKIN and a composition comprising PKIN antagonist is useful for treating  
 CC a disease or condition associated with overexpression of PKIN. The  
 CC disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,  
 CC myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder  
 CC (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,  
 CC autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes  
 CC mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,  
 CC osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,  
 CC rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,  
 CC bacterial, parasitic, fungal, viral, protozoal and helminthic infections)  
 CC growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,  
 CC Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio  
 CC vascular disease (arteriovenous fistula, hypertension, vasculitis,  
 CC aneurysms, congestive heart failure, angina pectoris, myocarditis,  
 CC ischaemic heart disease, chronic bronchitis, lung tumours); lipid  
 CC disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,  
 CC hypcholesterolaemia, obesity). PKIN DNA is useful for assessing  
 CC toxicity of a test compound and in gene therapy. The present sequence  
 CC is human PKIN-22 cDNA. Human PKIN-22 gene is located on chromosome 10.  
 XX  
 SQ Sequence 1880 BP; 454 A; 558 C; 505 G; 363 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 3,19e-198 Length: 1880  
 Score: 2241.00 Matches: 437  
 Percent Similarity: 79.56% Conservative: 34  
 Best Local Similarity: 73.82% Mismatches: 41  
 Query Match: 82.54% Indels: 80  
 DB: 24 Gaps: 5  
 US-09-820-790B-2 (1-516) x AAD26469 (1-1880)  
 QY 1 MetaAlaThrThrValThrCysThrArgPheThrAspGluTyrrGlnLeuTyrrGluAspIle 20  
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 Db 83 ATGGCCACCCAGCGCCACCTGACCGCGTTTCCAGGAGCTACACGCTCTTCGAGGAGCTT 142  
 QY 21 GlyTysGlyAlaPheSerValValArgArgCysValLysLeuCysThrGlyHisGluTyrr 40  
 |||||  
 Db 143 GGCAGGGTGTCTTCTCTGTGTGTCGCGAGGTGTGTGAAGAAACCTCCAGCAGGAGTAC 202  
 QY 41 AlaAlaLysIleIleAlaAsnThrLysLysLeuSerAlaArgAspHisGlnLysLeuGluArg 60

Db 203 GCACAAATCATCAATACCAAGAAATGTCGCCGGGATCCACCAAGACATAGAACCT 262  
 QY 61 GluAlaArgIleCysArgLeuLeuLysHisSerAsnIleValArgLeuHisAspSerIle 80  
 Db 263 GAGGCTGGATATGTCGACTTCTGAACATCCAAACATCGTGGCCCTCCATGACATATT 322  
 QY 81 SerGluGluGlyPheHisTyrLeuValPheAspLeuValThrGlyGlyGluLeuPheGlu 100  
 Db 323 TCTGAAGAGGGTTTCACTACCTGCTGTTTGAACCTTGTACCGGGGGAGCTGTTTGA 382  
 QY 101 AspIleValAlaArgGluTyrTyrSerGluAlaAspAlaSerHisCysIleGlnGlnIle 120  
 Db 393 GACATTGTGCCAGAGATCTACAGTGAAGCAGAGTCCAGCCACTGTATACATCAGATT 442  
 QY 121 LeuGluAlaValLeuHisCysHisGlnMetGlyValValHisArgAspLeuLysProGlu 140  
 Db 443 CTGGAGAGCTTTAAACCATCCACCATGACATGCTCCACAGGAGCCTGAAGCCTGAG 502  
 QY 141 AsnLeuLeuLeuAlaSerIleCysIleGlyValAlaValLysLeuAlaAspPheGlyLeu 160  
 Db 503 AACCTGCTGTCGCGAGTAAATGCAAGGGTCCCGCTCAAGCTGCTGATTTGGCCTA 562  
 QY 161 AlaIleGluValGlnGlyAspGlnAlaThrPheGlyPheAlaClyThrProGlyTyr 180  
 Db 563 GCCATCAAGTACAGGAGAGCAGCAGCTGTGGTTTGTCTGGCACCACCCAGGTAC 622  
 QY 181 LeuSerProGluValLeuArgLysGluAlaTyrGlyLysProValAlaIleThrAlaCys 200  
 Db 623 TTGTCCTCTGAGTCTGTGAGAAAGATCCCTATGGAACCTGTGGATATCGGGCTGC 682  
 QY 201 GlyValIleLeuTyrIleLeuLeuValGlyTyrProProPheTyrAspLysAspGlnHis 220  
 Db 683 GGGGTATCTGTATATCTCTGCTGGCTATCTCTCTCTGGATGAGATCAGCAC 742  
 QY 221 LysLeuTyrGlnGlnIleLysAlaClyAlaTyrAspPheProSerProGluTyrAspThr 240  
 Db 743 AAGCTGTATCAGCAGATCAAGCTGGAGCTGATGATTTGCCATCAACAGATGGACAC 802  
 QY 241 ValThrProGluAlaLysAsnLeuIleAsnGlnMetLeuThrIleAsnProAlaLysArg 260  
 Db 803 GTAATCTCTGAACCAAGAACTTGATCAACCAAGATGCTGACCATAAACCCAGCAAGCGC 862  
 QY 261 IleThrAlaHisGluAlaLeuLysHisProTyrValCysGlnArgSerThrValAlaSer 280  
 Db 863 ATCAGCGCTGACCAAGCTCTCAAGTACCCGTGGGTCTGTCAAGATCCACGCTGGCATCC 922  
 QY 281 MetMetHisArgGlnGluThrValGluCysLeuLysLysPheAsnAlaArgArgLysLeu 300  
 Db 923 ATGATGTCATCTCAGAGACTGTGGAGTGTGTGGCAAGTTCATGCTCCCGGAGAAACTG 982  
 QY 301 LysGlyAlaIleLeuThrThrMetLeuAlaThrArgAsnPheSerValGlyArgGlnThr 320  
 Db 983 AAGGTCCTCTCCAGCACCCTGCTCTCCAGGACTTCTCAGTGGCAGCAGCAGC 1042  
 QY 321 ThrAlaProAlaThrMetSerThrAlaAlaSerGlyThrThrMetGlyLeuValGlnGln 340  
 Db 1043 TCCGCCCGCGCTGCGCTGCGCAGCGCGCGCTGGCC-----GGCAAGCT 1093  
 QY 341 AlaLysSerLeuLeuAsnLysLysAlaAspGly----- 351  
 Db 1094 GCCAAAGCCCTATTGAACAGAAAGTCCGATGGCGGTCTCAAGAAAGGAATCGAGTTC 1153  
 QY 352 -----ValLysProGlnThrAsnSerThrLysAsnSerAlaAlaThrSerPro 368  
 Db 1154 ACGCTGCACCTATATGCCACAGACCAACAC---AAACACAGTCTCGTAGCCAGCCCAA 1210  
 QY 369 LysGlyThrLeuProProAlaAlaLeuGluProGlnThrThrValIleHisAsnProVal 388  
 Db 1211 GAGCCCGCGCGCTTGCAGAGCGGCCATGGAGCCACAAACCACTGTGTATACAAAGCTACA 1270  
 QY 389 AspGlyIleLysGluSerSerAlaAsnThrThrIleGluAspSerAlaLys 408

Db 1271 GATGGGATCAAGGGCTCCACAGAGAGCTCAACACCACCAAGAGATGAGGACCTCAA 1330  
 QY 409 Ala----- 409  
 Db 1331 GCTCCCCCGCTCCGCACTGGGAATGAGCAGCTGGTCTGCTGAAGACGAGACTCCCGGAC 1390  
 QY 410 -----Arg 410  
 Db 1391 AGAACAGCCCCCTGFCAGGAGATGCAAGCCCCAGCCCTTCTCTCTCTCCTCAGCCATGCGA 1450  
 QY 411 LysGlnGluIleIleLysThrThrGluGlnLeuIleGluAlaValAsnAsnGlyAspPhe 430  
 Db 1451 AAACAGGAGATCATTAAGATTACAGAACAGCTGATTGAAGCATCAACATGGGACTTT 1510  
 QY 431 GluAlaTyrAla----- 434  
 Db 1511 GAGGCTATACAGAGATTGTGATCCAGGCGCTCACTTCTTTGAGCCCTGAGGCCCTTGGT 1570  
 QY 435 -----PheTyrPheGluAsnLeuLeuAlaLysAsn 444  
 Db 1571 AACCTCGTGGAGGGGATGGATTCCATAGTTTACTTTGAGAAATCTCTGTCCAGAAC 1630  
 QY 445 SerLysProIleHisThrThrIleLeuAsnProHisValHisValIleGlyGluAspAla 464  
 Db 1631 AGCAAGCCTATCATACATACCATCTCTAAACCCACACGCTCCACGCTGATTGGGGAGGACGA 1690  
 QY 465 AlaCysIleAlaTyrIleArgLeuThrGlnTyrIleAspGlyGlnGlyArgProArgThr 484  
 Db 1691 GCGTGATCGCTTACATCCGCTCACCACATCATGACGGGAGGGTGGCCCTCCGACC 1750  
 QY 485 SerGlnSerGluGluThrArgValThrPheHisArgArgAspGlyLysTyrPheGlnAsnValHis 504  
 Db 1751 AGCCAGTCAAGAGAGACCCGGTCTGCGACCGCTGGGATGGCAAGTGCTCAATGTCCAC 1810  
 QY 505 PheHisCysSerGlyAlaProValAlaProLeuGln 516  
 Db 1811 TATCACTGTCTAGGGGCCCCCTGCCGACCCGCTGCAG 1846  
 RESULT 7  
 ABK83805  
 ID ABK83805 standard; cDNA; 1793 BP.  
 AC ABK83805;  
 XX  
 XX 14-AUG-2002 (first entry)  
 XX Human cDNA differentially expressed in granulocytic cells #376.  
 DE Human; ss; granulocytic cell; DNA chip; bacterial infection;  
 KW viral infection; parasitic infection; protozoal infection;  
 KW fungal infection; sterile inflammatory disease; psoriasis;  
 KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;  
 KW cardiac reperfusion injury; renal reperfusion injury; ARDS;  
 KW adult respiratory distress syndrome; inflammatory bowel disease;  
 KW Crohn's disease; ulcerative colitis; periodontal disease;  
 KW granulocyte activation; chronic inflammation; allergy.  
 OS Homo sapiens.  
 XX  
 XX WO200228999-A2.  
 XX  
 XX 11-APR-2002.  
 XX  
 XX 03-OCT-2001; 2001WO-US30821.  
 XX  
 XX 03-OCT-2000; 2000US-237189P.  
 XX  
 XX (GENE-) GENE LOGIC INC.  
 XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;  
 XX WPI; 2002-435328/46.  
 XX



PI Detecting granulocyte activation by detecting differential expression  
 PT of genes associated with granulocyte activation, which serves as  
 PT diagnostic markers that is useful for monitoring disease states and  
 PT drug toxicity -

PS Claim 1; SEQ ID No 376; 114pp; English.

XX The invention relates to detecting (M1) granulocyte (GC) activation  
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by  
 CC DNA chip analysis as given in the specification, and comparing  
 CC the expression level to an expression level in an unactivated  
 CC GC, where differential expression of Gs is indicative of GCA.  
 CC Also included are modulating (M2) GAs by contacting GC with an agent  
 CC that alters the expression of at least one gene in Gs; (2) screening (M3)  
 CC for an agent capable of modulating GCA or an inflammation (especially  
 CC chronic) in a tissue, an allergic response in a subject, exposure of a  
 CC subject to a pathogen or sterile inflammatory disease using the  
 CC gene expression profile; (3) detecting (M4) an inflammation (especially  
 CC chronic) in a tissue, an allergic response in a subject, exposure of a  
 CC subject to a pathogen or sterile inflammatory disease, by detecting the  
 CC level of expression in a sample of the tissue of gene(s) from Gs, where  
 CC the level of expression of the gene is indicative of inflammation;  
 CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,  
 CC an allergic response in a subject, exposure of a subject to a pathogen  
 CC or sterile inflammatory disease, by contacting a tissue having  
 CC inflammation with an agent that modulates the expression of gene(s)  
 CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for  
 CC modulating GA; M3 is useful for screening an agent capable of modulating  
 CC GCA preferably in an inflammation in a tissue; M4 is useful for  
 CC detecting an inflammation (especially chronic) in a tissue, an allergic  
 CC response in a subject, exposure of a subject to a pathogen or sterile  
 CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,  
 CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal  
 CC reperfusion injury, ARDS, adult respiratory distress syndrome,  
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,  
 CC periodontal disease; also bacterial infection, viral infection, and  
 CC parasitic infection, protozoal infection, fungal infection and M5 is  
 CC useful for treating one of the above conditions. The present  
 CC sequence represents a gene differentially expressed in granulocytes.  
 CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 1793 BP; 450 A; 502 C; 470 G; 371 T; 0 other;

#### Alignment Scores:

Pred. No.:	3,15e-197	Length:	1793
Score:	2230.00	Matches:	430
Percent Similarity:	83.79%	Conservative:	25
Best Local Similarity:	79.19%	Mismatches:	36
Query Match:	82.14%	Indels:	52
DB:	24	Gaps:	4

US-09-820-790B-2 (1-516) x ABK83805 (1-1793)

QY	1	MetaAlaThrValThrCysThrArgp2heThrAspGluTyrgInLeuTyrgLuspile	20
DB	22	ATGCGCCACCCGCCACCTGACCGCTTCACCGAGCATCCACAGCTTCGAGAGAGCTT	81
QY	21	GlyLysGlyAlaPheSerValValArgArgCysValLysLeuCysThrGlyHisGluTy	40
DB	82	GGCAAGGTCCTCTCTGTCGTCGAGGTGTGTGAAGAAACCTCCACGAGGAGTAC	141
QY	41	AlaAlaIleIleAsnThrLysLysLeuSerAlaArgAspHisGlnLysLeuGluArg	60
DB	142	GCAGCAAAATCATCAATACCAAGATTGCTGCGCGGGATACCAAGAACTAGAACGT	201
QY	61	GluAlaArgIleCysArgLeuLysHisSerAsnIleValArgLeuHisAspSerIle	80
DB	202	GAGCTCGGATATGTCGACTTCTGAACATCCAAACATCCTGCGGCCCTCAGACAGTAT	261
QY	81	SerGluGluGlyPheHisTyrlLeuValPheAspLeuValThrGlyGlyGluLeuPheGlu	100

DB	262	TCGAGAGAGGGTTTCACTACCTCTGTTGACCTTGTACGGAGGGAGCTTTTGA	371
QY	101	AspIleValAlaArgGluTyrrSerGluAlaAspAlaSerHisCysIleGlnGlu	120
DB	322	GACATTGTGGCCAGAGAGTACTACAGTGAAGCAGATGCCAGCCACTGTATATCATCAGATT	381
QY	121	LeuGluAlaValLeuHisCysHisGlnMetGlyValValHisArgAspLeuLysProGlu	140
DB	382	CTGGAGAGTGTTAACCAATCCACACGATGACATGCTCCACAGGAGCTGAGCCCTGAG	441
QY	141	AsnLeuLeuLeuAlaSerLysCysLysGlyAlaAlaValLysLeuAlaAspPheGlyLeu	160
DB	442	AACTGTGCTGGCAGTAAATCAAGGTCGCCCGCTCAAGCTGGCTGATTGTGGCCTA	501
QY	161	AlaIleGluValGlnGlyAspGlnGlnAlaThrPheGlyPheAlaGlyThrProGlyTy	180
DB	502	GCATPCGAAGTCAGGAGAGCAGCAGCTTGGTTGGTTTCTGGCACCCTGAGTTAC	561
QY	181	LeuSerProGluValLeuArgLysGluAlaTyrgLysProValAspIleTrpAlaCys	200
DB	562	TTGTCCTCCCTGAGGTCTTGAGGAAAGATCCCTATGGAAAACCTGTGATATCTGGCCTGC	621
QY	201	GlyValIleLeuTyrlleLeuValGlyTyrrProPheTrpAspGluAspGlnHis	220
DB	622	GGGTCATPCTGTATATCTCTGTGGCTATCTCTCTCTGGGATGAGATCAGCAC	681
QY	221	LysLeuTyrgInGlnIleLysAlaGlyAlaTyrrAspPheProSerProGluTrpAspThr	240
DB	682	AGCTGTATCAGCAGATCAAGCTCGAGCTATGATTCCTCCATCACCAGATGGACAG	741
QY	241	ValThrProGluAlaLysAsnLeuLeasGlnMetLeuThrIleAsnProAlaLysArg	260
DB	742	GTAACTCTGAGCCAGAACCTTGATCAACAGATGTGACCATAAACCCAGCAAAAGCC	801
QY	261	IleThrAlaHisGluAlaLeuLysHisProTrpValCysGluArgSerThrValAlaSer	280
DB	802	ATCAGGCTGACAGGCTCTCAGCACCCCTGGTGTGTGTGTCACAGATCCACGGTGGATCC	861
QY	281	MetMetHisArgGlnGluThrValGluCysLeuLysLysPheAsnAlaArgArgLysLeu	300
DB	862	ATGATGCATCTGTCAGGAGATGTGGAGTGTGGCAGTCAATGCCCGGAGAAATCG	921
QY	301	LysGlyAlaIleLeuThrThrMetLeuAlaThrArgAsnPheSerValGlyArgGlnThr	320
DB	922	AAGGTGCCATCTCAGACCATGCTGTCTCCAGGAATCTCAGCT-----	969
QY	321	ThrAlaProAlaThrMetSerThrAlaAlaSerGlyThrThrMetGlyLeuValGluGln	340
DB	969	-----	969
QY	341	AlaLysSerLeuLeuAsnLysLysAlaAsp---GlyValLysProGlnThrAsnSerThr	359
DB	970	GCCAAAGCCTATTGAACAGAGTCGATGCGGTGTCAAGCCACAGACAGCAAC---	1026
QY	360	LysAsnSerAlaAlaAlaThrSerProLysGlyThrLeuProProAlaAlaLeuGluPro	379
DB	1027	AAAAACATCTCTGAAGCCCGCCAGCCGCCCTCTGAGACGGCCATGGAGCCA	1086
QY	380	GlnThrThrValIleHisAsnProValAspGlyIleLysGluSerSerAspSerAlaAsn	399
DB	1087	CAAACCATCTGTGTACACACGCTACAGATGGGATCAAGGGCTCCACAGAGAGTGCAC	1146
QY	400	ThrThrIleGluAspGluAspAlaLysAlaArgLysGlnGluIleIleLysThrGlu	419
DB	1147	ACCACCAAGATGAGGACCTCAAGTCGGAACACAGGAGATCATTAAGATTACAGAA	1206
QY	420	GlnLeuIleGluAlaValAsnAsnGlyAspPheGluAlaTyrrAla	434
DB	1207	CAGCTGATTGAGCCATCAACATGGGACTTTGAGGCTTACAGAGATTGTGATCCA	1266
QY	434	-----	434

Db 1267 GGCTCAGTCTCTTTGAGCTGAGGCGCTTGGTTAACTCGTGGAGGGGATGGATTCCAT 1326  
 QY 435 ---PhcTyrPheGluAsnLeuLeuAlaLysAsnSerLysProIleHisThrIleLeu 453  
 Db 1327 AAGTTTACTTTGGAATCTCTCTGTCACGAAGACAGCAAGCCTATCCATACACCATCTTA 1386  
 QY 454 AsnProHisValHisValIleGlyGluAspAlaAlaCysIleAlaTyrIleArgLeuThr 473  
 Db 1387 AACCCACAGCTCCAGTGAATGGGAGGAGCAGCGTGCATCGCTACATCCGGCTCAC 1446  
 QY 474 GluTyrIleAspGlyGlnGlyArgProArgThrSerGlnSerGlnGluThrArgValTrp 493  
 Db 1447 CAGTATCATCGAGCGGCGGCTGCGCTGCGACAGCCAGTCCAGAGAGACCCGGGTCTGG 1506  
 QY 494 HisArgArgAspGlyLysTrpGlnAsnValHisPheHisCysSerGlyAlaProValAla 513  
 Db 1507 CACCGTCGGGATGGCAAGTGGCTCAATGCTCACTATCACTATCACTATCACTATCA 1566  
 QY 514 ProLeuGln 516  
 Db 1567 CCGCTGCAG 1575

RESULT 8  
 AAK52574  
 ID AAK52574 standard; cDNA; 3015 BP.  
 XX AC AAK52574;  
 XX DT 06-NOV-2001 (first entry)  
 XX DE Human polynucleotide SEQ ID NO 2103.  
 XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorder; arthritis; inflammation; ss.  
 XX OS Homo sapiens.  
 XX WO200157190-A2.  
 XX PN 09-AUG-2001.  
 XX PD 09-AUG-2001.  
 XX PF 05-FEB-2001; 2001WO-US04098.  
 XX PR 03-FEB-2000; 2000US-0496914.  
 PR 27-APR-2000; 2000US-0560875.  
 PR 20-JUN-2000; 2000US-0596075.  
 PR 19-JUL-2000; 2000US-0620325.  
 PR 01-SEP-2000; 2000US-0654936.  
 PR 15-SEP-2000; 2000US-0663561.  
 PR 20-OCT-2000; 2000US-0693325.  
 PR 30-NOV-2000; 2000US-0728422.  
 XX (HYSE-) HYSEQ INC.  
 XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;  
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
 PI xue AJ, Yang Y, Wejhrman T, Goodrich R;  
 XX WPI; 2001-476283/51.  
 DR P-PSDB; AAM79441.  
 XX Nucleic acids encoding polypeptides with cytokine-like activities,  
 PT useful in diagnosis and gene therapy -  
 XX Claim 1; Page 4481-4482; 6221pp; English.  
 XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
 CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or

CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation.  
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666  
 CC (AAM80020) are omitted as the relevant pages from the sequence listing  
 CC were missing at the time of publication.  
 XX  
 SQ Sequence 3015 BP; 731 A; 799 C; 811 G; 674 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 6,48e-197 Length: 3015  
 Score: 2330.00 Matches: 430  
 Percent Similarity: 83.79% Conservative: 25  
 Best Local Similarity: 79.19% Mismatches: 36  
 Query Match: 82.14% Indels: 52  
 DB: 22 Gaps: 4

US-09-820-790B-2 (1-516) x AAK52574 (1-3015)

QY 1 MetaAlaThrValThrCysThrArgPheThrAspGluTyrGlnLeuTyrGluAspIle 20  
 Db 22 ATGGCCACCCAGCCGCACTGACCCGTTTCACGAGGACTACGAGCTTCGAGGAGCTT 81  
 QY 21 GlyLysGlyAlaPheSerValValArgCysValLysLeuCysThrGlyHisGluTyr 40  
 Db 82 GGCAGGGTGCTTCTCTGTGTCGCGAGGTGTGTGAAGAAAACTCCACGAGGAGTAC 141  
 QY 41 AlaAlaLysIleAsnThrLysLysLeuSerAlaArgAspHisGlnLysLeuGluArg 60  
 Db 142 GCAGCAAAATCATCAATACCAAGAGTGTCTGCGCGGATCACCAAGACATGAGACGT 201  
 QY 61 GluAlaArgIleCysArgLeuLeuLysHisSerAsnIleValArgLeuHisAspSerIle 80  
 Db 202 GAGGCTCGGATATGCTGACTTCTGAACATCCAAACATCGTGGCCCTCCATGACAGTAT 261  
 QY 81 SerGluGluGlyPheHisTyrLeuValPheAspLeuValThrGlyGlyGluLeuPheGlu 100  
 Db 262 TCTGAAGAAGGGTTTCACTACCTGTTTGAACCTGTGTACCGCGGAGCTGTTTGA 321  
 QY 101 AspIleValAlaArgGluTyrTyrSerGluAlaAspAlaSerHisCysIleGlnIle 120  
 Db 322 GACATGTGGCCAGAGAGTACTACAGTGAAGCAGAGTCCGCGCCTGTATACATCAGATT 381  
 QY 121 LeuGluAlaValLeuHisCysHisGlnMetGlyValValHisArgAspLeuLysProGlu 140  
 Db 382 CTGGAGAGTGTAAACCATCATCCACCATCATCGTCCACAGGAGCTCAAGCCCTGAG 441  
 QY 141 AsnLeuLeuAlaSerLysCysLysGlyAlaAlaValLysLeuAlaAspPheGlyLeu 160  
 Db 442 AACCTGCTGCTGGCAGTAAATGCAAGGTGCGCGCTCAAGCTGGCTGATTTTGGCCTA 501  
 QY 161 AlaIleGluValGlnGlyAspGlnGlnAlaTrpPheGlyPheAlaGlyThrProGlyTyr 180  
 Db 502 GCCATCGAAGTACAGGAGAGACGACGCTGTTGTTGTTGTTGTCGACCCAGCTTAC 561  
 QY 181 LeuSerProGluValLeuArgLysGluAlaTyrGlyLysProValAspIleTrpAlaCys 200  
 Db 562 TTGTCCTGAGGTCTTGGAGAAAGATCCCTATGAAAAACCTGTGGATATCTGGGCTGC 621  
 QY 201 GlyValIleLeuTyrIleLeuValGlyTyrProPheTrpAspGluAspGlnHis 220  
 Db 622 GGGGTATCTCTATATCTCTCTGGTGGCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 681  
 QY 221 LysLeuTyrGlnGlnIleLysAlaGlyValTyrAspPheProSerProGluTyrPaspThr 240  
 Db 682 AACCTGATACAGCAGATCAGGCTGGAGCTGATGATTTCCCATCAGCAAGTGGGACAG 741  
 QY 241 ValThrProGluAlaLysAsnLeuIleAsnGlnMetLeuThrIleAsnProAlaLysArg 260  
 Db 742 GTAACTCTCTGAAGCAAGAACTTGATCAACAGATGCTGACCAATAAACCCAGCAAGGCG 801

QY 261 IleThrAlaHisGluAlaLeuLysHisProTrpValCysGlnArgSerThrValAlaSer 280  
 DB 802 ATCAGGGTCCAGGCTCTCAAGACCCGCTGGTGTCTCAAGATCCACGCTGGCATCC 861  
 QY 281 MetMetHisArgGlnGlnThrValGluCysLeuLysPheAsnAlaArgGlyLeu 300  
 DB 862 ATGATGCACTCTCAGAGACTGTGGAGTGTGGCGAGTCTCAATCCCGGAGAACTG 921  
 QY 301 LysGlyAlaIleLeuThrThrMetLeuAlaThrArgAsnPheSerValGlyArgGlnThr 320  
 DB 922 AAGGGTGCATCTCTCAGACCATCTCTCTCCAGGAACCTCTCAGCT----- 969  
 QY 321 ThrAlaProAlaThrMetSerThrAlaAlaSerGlyThrMetGlyLeuValGluGln 340  
 DB 969 ----- 969  
 QY 341 AlaLysSerLeuLeuAsnLysLysAlaAsp---GlyValLysProGlnThrAsnSerThr 359  
 DB 970 GCCAAAGCCTATTGAACAGAGTGGATGGCGTGTCAAGCCACAGACGACAAAC--- 1026  
 QY 360 LysAsnSerAlaAlaAlaThrSerProLysGlyThrLeuProAlaAlaLeuGluPro 379  
 DB 1027 AAAACAGTCTCTGAAGCCACGACCCACAGAGCCCGCCCTTGACAGAGCCCATGGAGCA 1086  
 QY 380 GlnThrThrValIleHisAsnProValAspGlyIleLysGluSerSerAspSerAlaAsn 399  
 DB 1087 CAACCACTGTGTACACACGCTACAGATGGATCAAGGGCTCCACAGAGAGCTGCAAC 1146  
 QY 400 ThrThrIleGluAspGluAspAlaLysAlaArgLysGlnIleLysThrThrGlu 419  
 DB 1147 ACCACACAGAGATGAGGACCTCAAGTGCAGAAACAGGAGATCATTAAGATTACAGAA 1206  
 QY 420 GlnLeuIleGluAlaValAsnAsnGlyAspPheGluAlaThrAla----- 434  
 DB 1207 CAGCTGATGAGCCATCAACATGGGGACCTTTGAGGCCCTACAGAGATTGTGATCCA 1266  
 QY 434 ----- 434  
 DB 1267 GGCTCACTTCTTTGAGCTGAGGCGCTTGTGAACCTCGTGGAGGGGATGGATTCCAT 1326  
 QY 435 ---PheTyrPheGluAsnLeuLeuAlaLysAsnSerLysProIleHisThrIleLeu 453  
 DB 1327 AGTTTACTTTGAGATCTCTCTGTCACAGACAGACAGCTATCCATACCACTCCATA 1386  
 QY 454 AsnProHisValHisValIleGlyGluAspAlaAlaLysIleAlaTyrIleArgLeuThr 473  
 DB 1387 AACCCACACCTCCACGCTGATGGGAGAGCGAGCGTGCATCGCTACATCCGCTCAC 1446  
 QY 474 GlnTyrIleAspGlyGlnGlyArgProArgThrSerGlnSerGluThrArgValTrp 493  
 DB 1447 CAGTACATCGAGCGGAGGCTCGGCTCGCACAGGAGGAGAGAGAGAGAGAGAGAG 1506  
 QY 494 HisArgArgAspGlyLysTyrGlnAsnValHisPheHisCysSerGlyAlaProValAla 513  
 DB 1507 CACCGTCGGATGTCAGAGTGGCTCAATGTCTCATCTCATCTCATCTCATCTCAT 1566  
 QY 514 ProLeuGln 516  
 DB 1567 CCGCTGCAG 1575

RESULT 9

AAH99755

ID AAH99755 standard; cDNA; 3015 BP.

XX

AC AAH99755;

XX

DT 16-OCT-2001 (first entry)

XX

DE Human protein encoding cDNA sequence SEQ ID NO:590.

XX Human; cancer; ulcer; HIV infection; human immunodeficiency virus;

KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;

KW antibacterial; endocrine; cardiant; central nervous system; virucide;  
 KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;  
 KW antiagregant; haemostatic; vulnary; antilucer; osteopathic; eczema;  
 KW dermatological; antiatheric; antiasthmatic; antidiabetic; cytostatic;  
 KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;  
 KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;  
 KW antiaphyllactic; rheumatoid arthritis; septic shock; pancreatitis;  
 KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;  
 KW genetic disease; haematopoietic disorder; platelet disorder; asthma;  
 KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;  
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;  
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;  
 KW neurological disorder; ss.

OS Homo sapiens.

XX WO200153455-A2.

XX 26-JUL-2001.

XX 22-DEC-2000; 2000WO-US35017.

XX 23-DEC-1999; 99US-0471275.

PR 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac R;

XX WPI; 2001-457603/49.

DR P-PSDB; AAH25814.

XX Isolated human polynucleotides encoding polypeptides, useful for the

XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection -

XX Claim 1; Page 628-629; 1217pp; English.

XX AAH99166 to AAH99904 encode the human proteins given in AAH25225 to

XX AAH25963. The proteins can have activities based on the tissues and

XX cells they are expressed in, such as: antiinflammatory; antirheumatic;

XX antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;

XX central nervous system; virucide; anti-HIV; fungicide; antimutagen;

XX cardiovascular; antianaemic; antiagregant; haemostatic; vulnary;

XX antilucer; osteopathic; dermatological; antiatheric; antiasthmatic;

XX antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;

XX antiparkinsonian; and immunostimulant. The proteins and polynucleotides

XX encoding them can be used in gene therapy, antisense therapy and vaccine

XX production, the proteins and polynucleotides are useful for screening for

XX agonists or antagonists of a protein and for the treatment and diagnosis of

XX disorders associated with the activity of a protein e.g. inflammation,

XX rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,

XX neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal

XX infections, autoimmunity, genetic diseases, haematopoietic disorders,

XX anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,

XX osteoporosis, severe combined immunodeficiency, eczema, allergic

XX rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,

XX Alzheimer's disease, Parkinson's disease, neurodegenerative and

XX neurological disorders.

XX Sequence 3015 BP; 731 A; 799 C; 811 G; 674 T; 0 other;

SQ

Alignment Scores:

Pred. No.: 6,48e-197 Length: 3015

Score: 2230.00 Matches: 430

Percent Similarity: 83.79% Conservative: 25

Best Local Similarity: 79.19% Mismatches: 36

Query Match: 82.14% Indels: 52

DB: 22 Gaps: 4

US-09-820-790B-2 (1-516) x AAH99755 (1-3015)

QY 1 MetalArThrValThrCysThrArgPheThrAspGlyTrcGlnLeuTyrGluAspIle 20







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Db 773 AAGCTGTATCAGCAGATCAAGGCTGGAGCCTATGATTTCCATCACCAGATGGACAG 832
QY 241 ValThrProGluAlaLysAsnLeuIleAsnGlnMetLeuThrIleAsnProAlaLysArg 260
Db 833 GTAACCTCTGAAGCAAGACTTGTATCAACACCATGCTGACCATAAACCCAGCAAGGCG 892
QY 261 IleThrAlaHisGluAlaLeuLysHisProTrpValCysGlnArgSerThrValAlaSer 280
Db 893 ATCAGCGCTGAGCGGCTCTCAAGCACCGCTGGGCTGTCAACAGTCCACGGTGGCATCC 952
QY 281 MetMetHisArgGlnGluThrValGluCysLeuLysLysPheAsnAlaArgLysLeu 300
Db 953 ATGATCATCTGTCAGGAGACTGTGGAGTGTTCGCCAAGTTCAATGCCGGAGAAAACATG 1012
QY 301 LysGlyAlaIleLeuThrThrMetLeuAlaIleThrArgAsnPheSerValGlyArgGlnThr 320
Db 1013 AAGGTTGCATCTCCAGACATGCTGTCTCCAGAACTTCTCAGTGGCAGGAGGAGC 1072
QY 321 ThrAlaProAlaThrMetSerThrAlaLeuSerGlyThrThrMetGlyLeuValGluGln 340
Db 1073 TCGCGCCCGCTCGCCTGGCGGAGCGCGCGCGCTGGCC-----GGGCAAGCT 1123
QY 341 AlaLysSerLeuLeuAsnLysLysAlaAsp---GlyValLysProGlnThrAsnSerThr 359
Db 1124 GCCAAAGCCATTGAACAAGATCGGATGGCGGTGTCAAGAAAAGGAAGTCGAGTTCC 1183
QY 360 LysAsnSerAlaAlaIleThrSerProLysGlyThrLeuProAlaAlaLeuGluPro 379
Db 1184 AGC-----GTGCACCTAATGGAGCCA 1204
QY 380 GlnThrThrValIleHisAsnProValAspGlyIleLysGluSerSerAlaAsn 399
Db 1205 CAAACACCTGTGTACACAGCTACAGATGGATCAAGGGCTCCACAGAGAGTGCAC 1264
QY 400 ThrThrIleGluAspGluAspAlaLysAla----- 409
Db 1265 ACCACCAAGATGAGGAGCCTCAAGCTGCCCGCTCGCACTGGGAATGGCAGCTCG 1324
QY 409 ----- 409
Db 1325 GTCCCTGAGGAGCGAGCTCCGGGACAGACAGCCCTCTCGAGCATGCGAGCCCGAG 1384
QY 410 -----ArgLysGlnGluIleLysThrThrGluGlnLeu 421
Db 1385 CCTCTCTCTCTCCTCAGCCATCGGAAACAGAGATCATTAAGATTACAGACAGCTG 1444
QY 422 IleGluAlaValAsnAsnGlyAspPheGluAlaIleValAla----- 434
Db 1445 ATTGAGCATCATCAATGGGACTTTGAGGCTTACAGCAAGATTGTGATCCAGGCTC 1504
QY 435 -----Phe 435
Db 1505 ACTTCTTTGAGCCTGAGCCCTTGGTAACTCTGGAGGGGATGGATTTCATAGTTT 1564
QY 436 TyrPheGluAsnLeuLeuAlaLysAsnSerLysProIleHisThrThrIleLeuAsnPro 455
Db 1565 TACTTTGAGAAATCTCTGTCCAGAGACAGACAGACCTATCATACCACCAATCTTAACCCA 1624
QY 456 HisValHisValIleGlyGluAspAlaAlaCysIleAlaIleArgLeuThrGlnTyr 475
Db 1625 CAGGTCCAGCTGATTGGGAGGAGCGAGCGGTGCTATCGCTACATCCGCTCACCAGTAC 1684
QY 476 IleAspGlyGlnGlyArgProArgThrSerGlnSerGluGluThrArgValTrpHisArg 495
Db 1685 ATCGAGGCGAGGTCGGCTTCGACCCAGCCAGTCAAGAGACCGGGTCTGGCACCGT 1744
QY 496 ArgAspGlyLysTrpGlnAsnValHisPheHisCysSerGlyAlaProValAlaProLeu 515
Db 1745 CGGGATGGCAAGTGGCTCATGTCCACTATCACTGCTCAGGGGCGCCCTGCCGACCGCTG 1804
QY 516 Gln 516
Db 1805 CAG 1807
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## RESULT 12

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AAK51590
XX AAK51590 standard; cDNA; 3026 BP.
XX
AC AAK51590;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 135.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Dmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
WPI: 2001-476283/51.
P-PSDB; AAK78457.
XX
Nucleic acids encoding polypeptides with cytokine-like activities,
useful in diagnosis and gene therapy -
Claim 1; Page 813-816; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAK7833-AAK80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAK80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 3026 BP; 733 A; 807 C; 812 G; 674 T; 0 other;
Alignment Scores:
Pred. No.: 3,61e-196 Length: 3026
Score: 2222.00 Matches: 429
Percent Similarity: 83.61% Conservative: 25
Best Local Similarity: 79.01% Mismatches: 37
Query Match: 18.84% Indels: 52
DB: 22 Gaps: 4
US-09-820-790B-2 (1-516) x AAK51590 (1-3026)
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QY 1 MetAlaThrThrValThrCysThrArgPheThrAspGluTyrGlnLeuTyrGluAspIle 20  
 Db 32 ATGGCCATCACCGCCACCTGACCCGCTTTTCCAGCGAGTACACAGCTCTTCGAGGAGCTT 91  
 QY 21 GlyTyrGlyAlaPheSerValValArgCysValLysLysLeuTyrGlyHisGluTyr 40  
 Db 92 GGCAGAGGCTCTTCTCTGTGTCGCGAGGAGTGTGAAGAAACCTCCAGCGAGAGTAC 151  
 QY 41 AlaAlaLysIleIleAsnThrLysLysLeuSerAlaArgAspHisGlnLysLysLeuGluArg 60  
 Db 152 GCGCAAAATCATCAATACCAAGAGTGTCTGCGCGGATCCACCGAGAACTAGAACCT 211  
 QY 61 GluAlaArgIleCysArgLeuLeuLysHisSerAsnIleValArgLeuHisAspSerIle 80  
 Db 212 GAGCTCGGATATGTGATCTCTGAAACATCCAAACATCGTCGCGCTCCATGACAGTAT 271  
 QY 81 SerGluGluGlyPheHisTyrLeuValPheAspLeuValThrGlyGlyGluLeuPheGlu 100  
 Db 272 TCTGAGAGGGTTTCACTACCTCGTGTGACCTTGTACGGAGGGAGCTGTGTGA 331  
 QY 101 AspIleValAlaArgGluTyrTyrSerGluAlaAspAlaSerHisCysIleGlnGlnIle 120  
 Db 332 GACATTTGTGCGCAGAGTACTACAGTGAAGCAGATGCCAGCCACTGTATACATCAGATT 391  
 QY 121 LeuGluAlaValLeuHisCysHisGlnMetGlyValValHisArgAspLeuLysProGlu 140  
 Db 392 CTGGAGAGTGTAAACCATCATCCACCATGACATGCTCCACAGGGAGCTGAGCCCTGAG 451  
 QY 141 AsnLeuLeuLeuAlaSerLysCysGlyAlaAlaValLysLeuAlaAspPheGlyLeu 160  
 Db 452 AACCTGTGCTGCGAGTAAATGCAAGGTTGCGCGCTCAAGCTGGCTGATTTTGGCCTA 511  
 QY 161 AlaIleGluValGlnGlyAspGlnAlaIleThrPheGlyPheAlaGlyThrProGlyTyr 180  
 Db 512 GCCATCAAGATAGAGGAGCAGCAGGCTTGGTTTGGTTTCTGGCCACCCAGGTTAC 571  
 QY 181 LeuSerProGluValLeuArgLysGluAlaTyrGlyLysProValAspIleTyrPalaCys 200  
 Db 572 TTGTCCCTCAGGCTTTGAGGAAGATCCCTATGATAAACCTGTGGATATCTGGCCCTGC 631  
 QY 201 GlyValIleLeuTyrIleLeuLeuValGlyTyrProPheTyrAspGluAspGlnHis 220  
 Db 632 GGAGTCACTCTGTATATCTCTGTTGGGCTATCTCTCTCTGAGATGAGGATCAGCAC 691  
 QY 221 LysLeuTyrGlnGlnIleLysAlaGlyValArgPheProSerProGluTyrAspThr 240  
 Db 692 AAGCTGTATCAGCAGATCAGGCTGAGCTTATGATTTCCATCACCAGATGGGACAG 751  
 QY 241 ValThrProGluAlaLysAsnLeuIleAsnGlnMetLeuThrIleAsnProAlaLysArg 260  
 Db 752 GTAACCTCTGAAGCCAAAGAACTTGATCAACCATGCTGACCATAAACCCAGCAAGCGC 811  
 QY 261 IleThrAlaHisGluAlaLeuLysHisProTyrValCysLysArgSerThrValAlaSer 280  
 Db 812 ATCAGGCTGACCAAGGCTCTCAAGCACCCGTTGCTGCTCAACGATCCAGCTGGCATCC 871  
 QY 281 MetMetHisArgGlnGluThrValGluCysLeuLysLysPheAsnAlaArgArgLysLeu 300  
 Db 872 ATGATGATCTCTCAGGAGACTGTGGAGTGTGGCACTTCAATGCCCGGAGAAACTG 931  
 QY 301 LysGlyAlaIleLeuThrThrMetLeuAlaThrArgAsnPheSerValGlyArgGlnThr 320  
 Db 932 AAGGTTGCTCATCTCAGCAGCATGCTTGTCTCCAGGAACCTCTCTCAGCT----- 979  
 QY 321 ThrAlaProAlaThrMetSerThrAlaAlaSerGlyThrThrMetGlyLeuValGluGln 340  
 Db 979 ----- 979  
 QY 341 AlaLysSerLeuLeuAsnLysLysAlaAsp---GlyValLysProGluThrAsnSerThr 359  
 Db 980 GCCAAAGCCCTATTGAACAGAGTCCGATGGCGGTCTCAAGCCACAGCAACAC--- 1036

QY 360 LysAsnSerAlaAlaAlaThrSerProLysGlyThrLeuProAlaAlaLeuGluPro 379  
 Db 1037 AAAAACAAGCTCTGTAAGCCCAAGAGAGCCCGGCGCTTGCAGAGCGCCATGAGGCA 1096  
 QY 380 GlnThrThrValIleHisAsnProValAspGlyIleLysGluSerSerAspSerAlaAsn 399  
 Db 1097 CAACACCTGTGTGTACACACGCTACAGATGGATCAAGGCTCCACAGAGCTGCAAC 1156  
 QY 400 ThrThrIleGluAspGluAspAlaLysAlaArgLysGlnGlnIleLysThrThrGlu 419  
 Db 1157 ACCACCAAGAGATGAGGAGCTCAAAAGTCGAAACAGAGAGATCAATAGATTACAGAA 1216  
 QY 420 GlnLeuIleGluAlaValAsnAsnGlyAspPheGluAlaTyrAla----- 434  
 Db 1217 CAGCTGATTGAAGCCATCAACATGGGACTTTGAGGCTACACGAAGATTGTGATCCA 1276  
 QY 434 ----- 434  
 Db 1277 GGCTCCTCCTTCTTGTAGCCCTGAGGCGCTTGTGTAACCTCTGTGAGGGAGTATTCAT 1336  
 QY 435 ---PheTyrPheGluAsnLeuAlaLysAsnSerLysProIleHisThrThrIleLeu 453  
 Db 1337 AAGTTTACTTTGAGAATCTCTCTGTCAGAAACAGAGAGCTATCCATACCCATCCCTA 1396  
 QY 454 AsnProHisValHisValIleGlyGluAspAlaAlaCysIleAlaTyrIleArgLeuThr 473  
 Db 1397 AACCACACCTCCACGTCGATTGGGGAGGAGCGAGCGTGCATCGCTACATCCGCTCACC 1456  
 QY 474 GlnTyrIleAspGlyGlnGlyArgProArgThrSerGlnSerGluGluThrArgValTyr 493  
 Db 1457 CAGTATCATCGAGCGGCGGCTCGGCTCCGACAGCCAGTCCAGAGAGACCCGGGCTGG 1516  
 QY 494 HisArgArgAspGlyLysTyrPglAsnValHisPheHisCysSerGlyValProValAla 513  
 Db 1517 CACGTCGGGATGCGAATGCTGCTCATATGCTCCATGCTCAGGGGCGCTGCCGCA 1576  
 QY 514 ProLeuGln 516  
 Db 1577 CCGCTGCAG 1585  
 RESULT 13  
 ABX63227  
 ID ABX63227 standard; cDNA; 3705 BP.  
 XX  
 AC ABX63227;  
 XX  
 DT 25-FEB-2003 (first entry)  
 XX  
 DE Human cDNA #227 differentially expressed in activated vascular tissue.  
 XX  
 KW Human; gene; ss; vascular tissue; cytostatic; atherosclerosis;  
 KW cardiant; hypotensive; antidiabetic; gynaecological; vasotropic;  
 KW cerebroprotective; gene therapy; vascular disease; cancer; coronary;  
 KW artery disease; hypertension; diabetes; pre-eclampsia; restenosis;  
 KW ischaemia-reperfusion injury; stroke;  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002137081-A1.  
 XX  
 PD 26-SEP-2002.  
 XX  
 PF 08-JAN-2002; 2002US-0044090.  
 XX  
 PR 28-JUL-2000; 2000US-222469P.  
 PR 08-JAN-2001; 2001US-260483P.  
 XX  
 PA (BAND/) BANDMAN O.  
 XX  
 PI Bandman O;  
 XX  
 DR WPI; 2003-110597/10.  
 XX



PT Combination for diagnosing, staging, treating, or monitoring the  
PT progression of treatment of a vascular disease, e.g. atherosclerosis,  
PT comprises several cDNAs that are differentially expressed in activated  
PT vascular tissue--  
XX

Claim 1; Page -: 18pp; English.

XX This invention relates to a combination comprising several cDNAs that  
CC are differentially expressed in activated vascular tissue. The invention  
CC also discloses a high throughput method for detecting differentially  
CC expressed cDNAs in a sample. The cDNAs of the invention may have  
CC antiatherosclerotic; cytostatic; cardiatic; hypotensive; antidiabetic;  
CC synecological; vasotropic and cerebroprotective activities and may be  
CC used in gene therapy. The cDNAs of the invention may be used in a  
CC high-throughput methods for detecting differential expression of one or  
CC more cDNAs in a sample, or screening several molecules or compounds to  
CC identify a molecule or compound that specifically binds a cDNA of the  
CC invention. A protein encoded by the cDNA may be used to screen several  
CC molecules or compounds to identify a ligand that specifically binds to  
CC the protein, or to produce or purify an antibody to the protein that can  
CC be used to detect a protein in a sample or purify a natural or  
CC recombinant protein from a sample. The nucleotides may be useful for  
CC diagnosing, staging, treating, or monitoring the progression of  
CC treatment of a vascular disease, e.g. atherosclerosis, cancer, coronary  
CC artery disease, hypertension, diabetes, pre-eclampsia, ischaemia-  
CC reperfusion injury, restenosis, or stroke. The cDNAs can also be used  
CC for large-scale genetic or gene expression analysis of several new  
CC nucleic acid molecules. Antibodies to the proteins encoded by the  
CC cDNAs are useful for diagnosing pre-pathologic disorders, and chronic  
CC or acute diseases associated with abnormalities in the expression,  
CC amount or distribution of the protein. The present sequence  
CC represents a cDNA of the invention that is differentially expressed in  
CC activated vascular tissue.

CC Note: The sequence data for this patent did not form part of the  
CC specification, but was obtained in electronic format directly from USPTO  
CC at <http://seqdata.uspto.gov/sequence.htm?docid=20020137061>.

XX Sequence 3705 BP; 901 A; 961 C; 970 G; 873 T; 0 other;

Alignment Scores:  
Pred. No.: 9.5e-193 Length: 3705  
Score: 2186.50 Matches: 421  
Percent Similarity: 81.18% Conservative: 19  
Best Local Similarity: 77.68% Mismatches: 29  
Query Match: 80.53% Indels: 73  
DB: 25 Gaps: 3

US-09-820-790B-2 (1-516) x ABX63227 (1-3705)

QY 1 MetAlaThrValThrCysThrArgPheThrAspGluTyrGlnLeuTyrGluAspIle 20  
DB 83 ATGGGCCACCCACCCACCTGCGACCGGTTTCCAGCAGACTACCAAGCTCTTCGAGGAGCTT 142  
QY 21 GlyLysGlyAlaPheSerValValArgCysValLysLeuCysThrGlyHisGluTyr 40  
DB 143 GSCAAGGTGCTTCTCTGTCGCGAGGTGTGTGAAGAAACCTCCACGAGGAGTAC 202  
QY 41 AlaAlaLysIleIleAsnThrLysLysLeuSerAlaArgAspHisGlnLysLeuGluArg 60  
DB 203 GCACGAAAAATCATCAATACCAAGAAATTTCTCGCCGGGATCATCAAGAACTAGAACGT 262  
QY 61 GluAlaArgIleCysArgLeuLeuLysHisSerAsnIleValArgLeuHisAspSerIle 80  
DB 263 GAGGCTCGATVATGTGCACTTCTGAACATCCCAACATCGTCGCGCTCCAGACAGTATT 322  
QY 81 SerGluGluGlyPheHisTyrLeuValPheAspLeuValThrGlyGlyGluLeuPheGlu 100  
DB 323 TCTGAGAGAGGGTTTCACTACCTCGTGTGTTGACCTGTTACCGCGGGGAGCTGTTTGA 382  
QY 101 AspIleValAlaArgGluTyrTyrSerGluAlaAspAlaSerHisCysIleGlnGlnIle 120  
DB 383 GACATTGTGGCCAGAGTACTACAGTGAAGCAGATGCCAGCCTACTGTATACATCAGATT 442

QY 121 LeuGluAlaValLeuLeuHisCysHisGlnMetGlyValValHisArgAspLeuLysProGlu 140  
DB 443 CTGGAGAGTGTAAACACACATCCACACGATCAGATCTCCACAGGAGCTGAAGCCCTGAG 502  
QY 141 AsnLeuLeuLeuAlaSerLysCysLysGlyAlaAlaValLysLeuAlaAspPheCysLeu 160  
DB 503 AACCTGCTGCTGGCGAGTAAATGCAAGGGTCCCGCTCAAGCTGCTGATTTGGCCCTA 562  
QY 161 AlaIleGluValGlnGlyAspGlnGlnAlaTrpPheGlyPheAlaGlyThrProGlyTyr 180  
DB 563 GCCATCGAAGTACAGGAGGAGCAGCAGCGCTTGGTGGTTGGTTGGTGGCACCAGGTTAC 622  
QY 181 LeuSerProGluValLeuLeuArgLysGluAlaTyrGlyLysProValAspIleTrpAlaCys 200  
DB 623 TTGTCCCTCGAGGTCTGGAGAAAGATCCCTATGGAACCTGTGATATCTGGGCTGTC 682  
QY 201 GlyValIleLeuTyrIleLeuLeuValGlyTyrProPheTrpAspGluAspGlnHis 220  
DB 683 GGGGTTCATCTGTATATCTCCTGGTGGCTATCTCCTCTCTGGGATGAGGATCAGCAC 742  
QY 221 LysLeuTyrGlnGlnIleLysAlaGlyAlaTyrAspPheProSerProGluTrpAspThr 240  
DB 743 AAGCTGTATCAGCAGATCAAGGCTGGAGCTGATGATTTCCATCCACAGATGGGACAG 802  
QY 241 ValThrProGluAlaLysAsnLeuIleAsnGlnMetLeuThrIleAsnProAlaLysArg 260  
DB 803 GTAACCTCTGAAGCCAGAACTTGATCAACAGATGCTGACCATTAACCCAGCAAGCGC 862  
QY 261 IleThrAlaHisGluAlaLeuLysHisProTrpValCysGlnArgSerThrValAlaSer 280  
DB 863 ATCAGCGCTGACAGGCTCTCAGCAGCCGCTGGTGTGTCAAGATTCACGATGCGATCC 922  
QY 281 MetMetHisArgGlnGlnThrValGluCysLeuLysLysPheAsnAlaArgArgLysLeu 300  
DB 923 ATGATGCTATCTGAGGAGACTGTGGAGGTTCGCAAGTTCAATGCCGGGAGAAACTG 982  
QY 301 LysGlyAlaIleLeuThrThrMetLeuAlaThrArgAsnPheSerValGlyArgGlnThr 320  
DB 983 AAGGTGTCATCTCCAGCACCATGCTGTCTCCAGAACTTCACGCT----- 1030  
QY 321 ThrAlaProAlaThrMetSerThrAlaAlaSerGlyThrThrMetGlyLeuValGluGln 340  
DB 1030 ----- 1030  
QY 341 AlaLysSerLeuLeuAsnLysLysAlaAspGlyValLysProGlnThrAsnSerThrLys 360  
DB 1031 GCCAAAGCCTATTGAACAAAGAGTCCGATGCG----- 1063  
QY 361 AsnSerAlaAlaAlaThrSerProLysGlyThrLeuProAlaAlaLeuGluProGln 380  
DB 1064 -----GGTCTCAAGGAGCCCAA 1081  
QY 381 ThrThrValIleHisAsnProValAspGlyLysLysGluSerSerAspSerAlaAsnThr 400  
DB 1082 ACCACTGTGGTACACACAGCTACAGATGGGATGAGGCTCCACAGAGACTGCAACACC 1141  
QY 401 ThrIleGluAspGluAspAlaLysAlaArgCysGlnGluIleLysThrThrGluGln 420  
DB 1142 ACCACAGAGATGAGGAGCTCAAGTCCGAAACAGAGGATCATTAGATTACAGACAG 1201  
QY 421 LeuIleGluAlaValAsnAsnGlyAspPheGluAlaTyrAla----- 434  
DB 1202 CTGATTGAAGCCATCAACATGGGACTTTGAGGCTACACAGAGATTTGTGATCCAGGC 1261  
QY 434 ----- 434  
DB 1262 CTCACCTTCCTTTGAGCCTGAGGCCCTTGGTAACTCTGAGGAGGATGATTTCCATAAG 1321  
QY 435 PheTyrPheGluAsnLeuLeuAlaLysAsnSerLysProIleHisThrThrIleLeuAsn 454  
DB 1322 TTTTACTTTGAGAAATCTCTGCCAAGACAGCAAGCCTATCCATACCACTCCATTAAC 1381  
QY 455 ProHisValHisValIleGlyGluAspAlaAlaCysIleAlaTyrIleArgLeuThrGln 474

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|||||
Db 1382 CCACAGCTCCAGTATCGGAGAGCGAGCGCTGATCGCTACATCCGCTCACCCAG 1441
QY 475 TyrIleAspGlyGlnGlyArgProArgThrSerGlnSerGluGluThrArgValTrpHis 494
Db 1442 TACATGACGGGCGAGGTCGGCTCGCACCCAGCCAGTCAGAGAGACCCGGGCTGGCAC 1501
QY 495 ArgArgAspGlyTrpGlnAsnValHisPheHisCysSerGlyAlaProValAlaPro 514
Db 1502 GGTGGGATGGCAAGTGGCTCAATGCTCACTATCACTGCTCAGGGGCCCTGCCGACGG 1561
QY 515 LeuGln 516
Db 1562 CTGCAG 1567

RESULT 14
ABK63630
ID ABK63630 standard; cDNA; 5637 BP.
XX
AC ABK63630;
XX
XX 18-JUN-2002 (first entry)
XX
XX Rat sequence differentially expressed in response to a hepatotoxin #1537.
XX
XX Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;
XX differential expression; centrilobular necrosis; steatosis.
XX
XX Rattus norvegicus.
XX
XX WO200210453-A2.
XX
XX 07-FEB-2002.
XX
XX 30-JUL-2001; 2001WO-US23872.
XX
XX 31-JUL-2000; 2000US-222040P.
XX 02-NOV-2000; 2000US-244880P.
XX 11-MAY-2001; 2001US-290029P.
XX 15-MAY-2001; 2001US-290645P.
XX 22-MAY-2001; 2001US-292336P.
XX 06-JUN-2001; 2001US-295798P.
XX 13-JUN-2001; 2001US-297457P.
XX 19-JUN-2001; 2001US-298884P.
XX 09-JUL-2001; 2001US-303459P.
XX
XX (GENE-) GENE LOGIC INC.
XX
XX Mendrick D, Porter MW, Johnson KR, Castle AL, Elashoff MR;
XX
XX WPI; 2002-241625/29.
XX
XX Predicting toxic effects of compounds or the progression of these toxic
XX effects by determining the changes in gene expression in tissues or
XX cells exposed to the toxin and comparing these to gene expression in
XX unexposed tissues or cells -
XX
XX Claim 1; Seq ID No 1537; 239pp; English.
XX
XX The invention relates to methods for predicting toxic effects of
XX compounds or the progression of these toxic effects by determining the
XX global changes in gene expression in tissues or cells exposed to the
XX toxin and comparing these to gene expression in unexposed tissues or
XX cells. Also included are methods of predicting at least one toxic
XX effect of a compound or progression of a toxic effect, preferably the
XX hepatotoxicity of a compound, comprising detecting the level of
XX expression in a tissue or cell sample exposed to the compound of two or
XX more genes listed in the specification, where differential expression of
XX the genes is indicative of at least one toxic effect or progression.
XX The method can also be used to identify an agent which modulates the
XX toxic response and predict cellular pathways that a compound modulates
XX in a cell. The methods utilise a set of at least two probes (on a solid
XX support in kit form), where each of the probes comprises a sequence that

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CC specifically hybridises to a gene listed in the specification, a computer system comprising a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising at least two genes listed in the specification, CC and a user interface to view the information used to present information, CC identifying the expression level in a tissue or cell of at least one gene listed in the specification. The method is useful for elucidating global changes in gene expression and for identifying toxicity markers in tissues or cell exposed to a known toxin. The genes may be used as toxicity markers in drug screening and toxicity assays. The genes and gene expression information may be used as diagnostic markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound or agent. Hepatotoxicity is characterised by centrilobular necrosis and steatosis. The present sequence is an expressed sequence tag (EST) or cDNA derived from a gene which is differentially expressed in response to a hepatotoxic agent.

XX Sequence 5637 BP; 1534 A; 1267 C; 1176 G; 1660 T; 0 other;

#### Alignment Scores:

Pred. No.: 1.3e-191 Length: 5637  
 Score: 2177.00 Matches: 420  
 Percent Similarity: 83.21% Conservative: 31  
 Best Local Similarity: 77.49% Mismatches: 35  
 Query Match: 80.18% Indels: 56  
 DB: 24 Gaps: 6

US-09-820-790B-2 (1-516) x ABK63630 (1-5637)

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QY 1 MetAlaThrValThrCysThrArgPheThrAspGluThrValGlnLeuArgAspIle 20
Db 223 ATGSGTTCGACCAACCACTGCACCGGTTCCACGGAGAGTATCAGCTCTTCGAGGAGCTC 282
QY 21 GlyYsGlyAlaPheSerValValArgArgCysValLysLeuCysThrGlyHisGluTyr 40
Db 283 GGAAGGGGGGCAATCTCAGTGTGAGAAGATGCAATGAGAAATCCCTACTGACAAAGATG 342
QY 41 AlaAlaLysIleIleAsnThrLysLysLeuSerAlaArgAspHisGlnLysLeuGluArg 60
Db 343 GCTGCCAAATATATCAACCAAAAGAGCTTCTGCTAGGATCATCAGAACTGGAAAGG 402
QY 61 GluAlaArgIleCysArgLeuLysHisSerAsnIleValArgLeuHisAspSerIle 80
Db 403 GAAGCTAGAAATCTGCGGCTCTTGAAGCACCCCAATATTTGAGACTTCATGACAGATA 462
QY 81 SerGluGluGlyPheHisTyrLeuValPheAspLeuValThrGlyGlyGluLeuPheGlu 100
Db 463 TCCGAAGAGGGGCTTCCATTACTTGGTGTGTGACTTAGTACTGTGGCGAAGCTTTTGAA 522
QY 101 AspIleValAlaArgGluTyrTyrSerGluAlaAspAlaSerHisCysIleGlnGlnIle 120
Db 523 GACATAGTGGCAAGAGAAATATACAGTGAGGCTGATGCCAGTCATTGTATACACAGATT 582
QY 121 LeuGluAlaValLeuHisCysHisGlnMetGlyValValHisArgAspLeuLysProGlu 140
Db 583 CTAGAGAGTGTAAATCAATTGTCACTAAATGGCANTAGTTCACAGGGACCTGGAAGCCTGAG 642
QY 141 AsnLeuLeuAlaSerLysCysLysGlyValAlaValLysLeuAlaAspPheGlyLeu 160
Db 643 AATTTGCTTTTAGCTAGCAAAATCCAAAGAGGAGCAGCTGTGAAGCTGGCAGACTTCGGCTTA 702
QY 161 AlaIleGluValGlnGlyAspGlnGlnAlaTrpPheGlyPheAlaGlyThrProGlyTyr 180
Db 703 GCCATAGAAGTTCAGGGCGACACAGCGGCGTGTGTTTGTGTTTGTGTCACACCTGGGAT 762
QY 181 LeuSerProGluValLeuArgLysGluAlaTyrGlyLysProValAspIleTrpAlaCys 200
Db 763 CTTTTCCTCCAGAGTCTCCTACGTAAAGATTCCTTATGGAACCAACAGTGGAGCTGGCATGT 822
QY 201 GlyValIleLeuTyrIleLeuValGlyTyrProPheTrpAspGluAspGlnHis 220
Db 823 GCGCTCATCTCTACATCTTCTGCTGGTGGGATACCCACCTTCTCTGGGATGAAGATCAGCAT 882

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121 GCTCCAAAATATCAACACCAAAAGCTTCTCGTAGGGATCATCAAAACATAGAAAGA 180
QY
61 GluAlaArgIleCysArgIleLeuLysHisSerAsnIleValArgLeuHisAspSerIle 80
181 GAAGCTAGAAATCTGGCGTCTTTTGAACACACCTTAATATTGTGCGACTTCATGATAGCATA 240
QY
81 SerGluGluGlyPheHisTyrLeuValPheAspLeuValThrGlyGlyGluLeuPheGlu 100
241 TCAGAGAGGGCTTTCACCTACTTGGTGTGTTGATTAGTTACTGGAGGTGAACCTGTGAA 300
QY
101 AspIleValAlaArgIleTyrSerGluAlaAspAlaSerHisCysIleGlnIle 120
301 GACATGTGCGAGAGATACACAGTGAAGCTGTGTCAGGTCATGATGACAGAGAT 360
QY
121 LeuGluAlaValLeuHisCysHisGlnMetGlyValValHisArgAspLeuLysProGlu 140
361 CTAGAAAGTCTTAATCATTGTCCACCTAAATGGCATAGTTCACAGGGACCTGAAGCCTGAG 420
QY
141 AsnLeuLeuLeuAlaSerIleCysGlyAlaAlaValLysLeuAlaAspPheGlyLeu 160
421 AATTGTCTTTAGCTAGCAAAATCCAAAGGGACAGCTGTGAATTTGGCAGACTTTGGCTTA 480
QY
161 AlaIleGluValGlnGlyAspGlnAlaThrPheGlyPheAlaGlyThrProGlyTyr 180
481 GCCATAGAGTTCAAGGGACACAGCGCTGGTGTGTTGCTGGGCACACCTGGGATAT 540
QY
181 LeuSerProGluValLeuArgLysGluAlaTyrGlyLysProValAlaPheTrpAlaCys 200
541 CTTTCTCCGAAGTTTTAGCTAAAGATCCTTATGGAAGCCAGTGGATATGTGGCATGT 600
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201 GlyValIleLeuTyrIleLeuLeuValGlyTyrProPheTrpAspGluAspGlnHis 220
601 GGTGTCAATCTCTATATTTACTTGTGGGTATCCACCCCTCTGGGATGAGACCAACAC 660
QY
221 LysLeuTyrGlnGlnIleLysAlaGlyAlaTyrAspPheProSerProGluTrpAspThr 240
661 AGACTCTATCAGCAGATCAAGCTGGAGCTTATGATTTCCATCCACAGATGGGACAG 720
QY
241 ValThrProGluAlaLysAsnLeuIleAsnGlnMetLeuThrIleAsnProAlaLysArg 260
721 GTGACTCCTGAGCCAAAGACCTCATCAATAAATGCTTACTATCAACCTGCCAAACGC 780
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261 IleThrAlaHisGluAlaLeuLysHisProTrpValCysGlnArgSerThrValAlaSer 280
781 ATCAGAGCTCAGAGGCACGTGAAGCACCCATGGATGTCAACGTTCTACTGTGTCTTC 840
QY
281 MetMetHisArgGlnGluThrValGluCysLeuLysLysPheAsnAlaArgArgLysLeu 300
841 ATGATGACACAGACAGAGAGACTGTAGACTGCTTGAAGAAATTAATGCTAGAGAAACTA 900
QY
301 LysGlyAlaIleLeuThrThrMetLeuAlaThrArgAsnPheSerValGlyArgGlnThr 320
901 AAGGSGCCATCTTGCAACTATGTGCTGACAGGAATTTCTCAGCA----- 948
QY
321 ThrAlaProAlaThrMetSerThrAlaAlaSerGlyThrThrMetGlyLeuValGluGln 340
948 ----- 948
QY
341 AlaLysSerLeuLeuAsnLysLysAlaAspGlyValLysProGlnThrAsnSerThrLys 360
949 GCCAAGAGTTTGTGAAGAACCA----- 972
QY
361 AsnSerAlaAlaAlaThrSerProLysGlyThrLeuProProAlaAlaLeuGluProGln 380
972 ----- 972
QY
381 ThrThrValIleHisAsnProValAspGlyIleLysGluSerSerAspSerAlaAsnThr 400
973 -----GATGAGTAAAGGAGTCAACTGAGAGTTCAAATACA 1008
QY
401 ThrIleGluAspGluAspAlaLysAlaArgLysGlnGluIleIleLysThrThrGluGln 420
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1009 ACATTTGACGATGAAGATGTGAAAGCACGAAGACGAGAGATTATCAAAGTCACTGAACAA 1068
QY
421 LeuIleGluAlaValAsnAsnGlyAspPheGluAlaTyrAla----- 434
1069 CTGATCGAAGCTATCAACAATGGGGACTTTGAAGCCTACACAAAAATCTGTGACCCAGGC 1128
QY
434 ----- 434
1129 CTTACTGCTTTTGAACCTGAAGCTTTGGGTAATTTAGTGAAGGGATGGATTTTCACCGA 1188
QY
435 PheTyrPheGluAsnLeuLeuAlaLysAsnSerLysProIleHisThrThrIleLeuAsn 454
1189 TTCTACTTTGAAAAATGCTTTGTCCAAAAGCAATAAACCACTATATTTCTTAAC 1248
QY
455 ProHisValHisValIleGlyGluAspAlaAlaCysIleAlaTyrIleArgLeuThrGln 474
1249 CCTCATGTACATCTGCTAGGGATGATGCCGCTGCATAGCATATATTAGGCTCACACAG 1308
QY
475 TyrIleAspGlyGlnGlyArgProArgThrSerGlnSerGluGluThrArgValTrpHis 494
1309 TACATGATGGCAGTGGAAATGCCAAAGACAAATGCAGTCAGAGAGACTCGTGTGGGCAC 1368
QY
495 ArgArgAspGlyLysTrpGlnAsnValHisPheHisCysSerGlyAlaProValAlaPro 514
1369 CGCGGGGATGAAAAGTGGCAGATGTTTCATTTTCATGCTGGGGTCCACCAACAGTACC 1428
QY
515 LeuGln 516
1429 ATCAAG 1434
QY
515 LeuGln 516
1429 ATCAAG 1434
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Search completed: October 10, 2003, 08:24:48  
Job time : 497 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 10, 2003, 08:11:37 ; Search time 3208 Seconds  
(without alignments)  
3909.323 Million cell updates/sec

Title: US-09-820-790B-2  
Perfect score: 2715  
Sequence: 1 MATTYTCRFFDEYQLYEDI.....DGKQNVHFCGAPVAPLQ 516

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters: -MODEL=frame+p2n.model -DEV=xlh  
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-LOCALALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09820790 -CGN\_1.1.2810 -runat\_09102003\_170019\_14775 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-XGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: em\_estba.\*
- 2: em\_esthum.\*
- 3: em\_estin.\*
- 4: em\_estmu.\*
- 5: em\_estov.\*
- 6: em\_estpl.\*
- 7: em\_estro.\*
- 8: em\_htc.\*
- 9: gb\_est1.\*
- 10: gb\_est2.\*
- 11: gb\_htc.\*
- 12: gb\_est3.\*
- 13: gb\_est4.\*
- 14: gb\_est5.\*
- 15: em\_estfun.\*
- 16: em\_estom.\*
- 17: em\_gss\_hum.\*
- 18: em\_gss\_inv.\*
- 19: em\_gss\_pln.\*
- 20: em\_gss\_vit.\*
- 21: em\_gss\_fun.\*
- 22: em\_gss\_mam.\*
- 23: em\_gss\_mus.\*
- 24: em\_gss\_pro.\*
- 25: em\_gss\_rod.\*
- 26: em\_gss\_phg.\*
- 27: em\_gss\_vrl.\*
- 28: gb\_gss1.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2663	98.1	3996	11	AK046454 Mus muscu
2	2504.5	92.2	1877	11	BC024803 Mus muscu
3	2224	81.9	3613	11	AK078311 Mus muscu
4	2204	81.2	2671	11	AK039076 Mus muscu
5	2186.5	80.5	3563	11	AK031213 Mus muscu
6	2076	76.5	1905	11	AK012702 Mus muscu
7	2012.5	74.1	4949	11	AK083245 Mus muscu
8	1907.5	70.3	3480	11	BC042895 Mus muscu
9	1698	62.5	1201	13	EX420151
10	1613	59.4	4207	11	AK032524 Mus muscu
11	1604.5	59.1	1374	11	BC022558 Homo sapi
12	1601	59.0	2132	11	AK081969 Mus muscu
13	1588	58.5	1201	13	EX445032
14	1582	58.3	2709	11	AK044872 Mus muscu
15	1534	56.5	934	13	EX420898
16	1519	55.9	1201	13	EX440674
17	1497	55.1	1201	9	AL553478
18	1496	55.1	954	9	AL537719
19	1452	53.5	1201	13	EX344742
20	1421.5	52.4	1201	13	EX460288
21	1413.5	52.1	866	14	CD515849
22	1403.5	51.7	1201	13	EX461065
23	1391	51.2	1005	13	EX344338
24	1391	51.2	1050	9	AL526517
25	1359	50.1	1201	13	EX445438
26	1356	49.9	1136	9	AL549926
27	1336	49.2	910	13	BQ933559
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33	1288	47.4	843	12	B1116053
34	1287	47.4	764	12	B1597219
35	1285	47.3	1201	9	AL539204
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39	1267	46.7	774	13	BQ179939
40	1265.5	46.6	1201	13	EX420474
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ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION Mus musculus adult male corpora quadrigemina cDNA, RIKEN  
3996 bp mRNA linear HTC 05-DEC-2002  
full-length enriched library, clone:B230386M10  
Product:CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II BETA  
CHAIN (CAM- KINASE II BETA CHAIN) (EC 2.7.1.123) (CAMK-II, BETA  
SUBUNIT), full insert sequence.  
ACCESSION AK046454  
VERSION AK046454.1 GI:26338100  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
92279253  
10349636

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
24993574  
11042159

3 Shibata, K., Itoh, M., Alizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861

4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Alizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L.M., Stauble, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bernaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, K., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombauts, P., Nordone, P., Ring, B., Schönbach, C., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schönbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409 (6821), 685-690 (2001)  
21085660  
11217851

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 3996)

7 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.go.jp/  
URL: http://fantom.gsc.riken.go.jp/.

FEATURES  
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BASE COUNT 884 a 1129 c 1130 g 853 t

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Pred. No.: 1.19e-277 Length: 3996  
Score: 2663.00 Matches: 509  
Percent Similarity: 94.46% Conservative: 3  
Best Local Similarity: 93.91% Mismatches: 4  
Query Match: 98.08 Indels: 26  
DB: 11 Gaps: 1

US-09-820-790B-2 (1-516) x AK046454 (1-3996)

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QY 21 GLYSGLYAlaPheSerValValArgCysValLysLeuCysThrGlyHisGluTyr 40  
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Db 272 GGCAAGGGGGCTTCTCTGTGTGGTGGCGACCTGTCTCAAGCTCTGTACCGCGCATGAGTAT 331  
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QY 41 AlaAlaLysIleIleAsnThrLysLysLeuSerAlaArgAspHisGlnLysLeuGluArg 60  
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QY      |||

RESULT 2
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LOCUS Mus musculus, Similar to calcium/calmodulin-dependent protein
DEFINITION kinase (Cam kinase) II beta, clone IMAGE:595935, mRNA.
ACCESSION BC024803.1 GI:19354130
VERSION BC024803.1
KEYWORDS HTC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Strausberg, R.
Direct Submission
Submitted (01-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Guanaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 54 Row: k Column: 21
This clone was selected for full length sequencing because it
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This clone has the following problem: frame shifted.

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US-09-820-790B-2 (1-516) x BC024803 (1-1877)
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DB 1008 -----CCCAAGAGTTTACTCAACAAGAACG 1033
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QY 369 sGlyThrLeuProAlaAlaLeuGluProGlnThrThrValIleHisAsnProValas 389
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## RESULT 3

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enriched library, clone:643059H15
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GAMMA-C PROTEIN KINASE II homolog [Sus scrofa], full insert
sequence.
ACCESSION AK078311
VERSION AK078311.1 GI:26347132
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning

```



JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

Meth. Enzymol. 303, 19-44 (1999)  
99279253  
10349636

2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
20499374

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

11042159

3

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, K., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipipillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

4

Kawai, J., Shingawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, P., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Buit, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection

Nature 409 (6821), 685-690 (2001)

21085660

11217851

5

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

6

(bases 1 to 3613)  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Soabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Ahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp).

COMMENT

URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: <http://genome.gsc.riken.go.jp/>URL: <http://fantom.gsc.riken.go.jp/>.

FEATURES

source

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polyA\_site

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Query Match: 81.92% Indels: 54  
DB: 11 Gaps: 5

US-09-820-790B-2 (1-516) x AK078311 (1-3613)

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LOCUS	Mus musculus adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A230093D17		
DEFINITION	product:calcium/calmodulin-dependent protein kinase II, delta, full insert sequence.		
ACCESSION	AK039076		
VERSION	AK039076.1	GI:26333028	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	1	Carninci, P. and Hayashizaki, Y.	
AUTHORS	High-efficiency full-length cDNA cloning		
TITLE	Meth. Enzymol. 303, 19-44 (1999)		
JOURNAL	9279253		
MEDLINE	10349636		
PUBMED			
REFERENCE	2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	
AUTHORS	Normalization and subtraction of cap-trapper-selected cDNAs to		
TITLE	prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE	3	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuda, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	
AUTHORS	RIKEN integrated sequence analysis (RISA) system-384-format		
TITLE	sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE	4	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamada, S., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Stauber, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,	

Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Marzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Sato, K., Schenbach, C., Seta, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilmshing, L., Yoshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection

Nature 409 (6821), 685-690 (2001)  
21085660  
11217851

#### REFERENCE

#### AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)  
6 (bases 1 to 2671)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koyda, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku, Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

#### TITLE

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/  
URL: http://fantom.gsc.riken.go.jp/

#### FEATURES

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
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 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning  
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 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
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 Normalization and subtraction of cap-trapper-selected cDNAs to  
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 Genome Res. 10 (10), 1617-1630 (2000)  
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 Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohtsuki, S.  
 and Hayashizaki, Y.  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409 (6821), 685-690 (2001)  
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 The FANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation  
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 Nature 420, 563-573 (2002)  
 6 (bases 1 to 3563)  
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 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
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 Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of

Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.  
 URL: <http://genome.gsc.riken.go.jp/>  
 URL: <http://fantom.gsc.riken.go.jp/>  
 Location/Qualifiers

#### FEATURES

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US-09-820-790B-2 (1-516) x AK031213 (1-3563)

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ORIGIN

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VERSION		AK083245.1	GI:26350378		
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ORGANISM		Mus musculus			
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AUTHORS		Carninci,P., and Hayashizaki,Y.			
TITLE		High-efficiency full-length cDNA cloning			
JOURNAL		Meth. Enzymol. 303, 19-44 (1999)			
MEDLINE		99279253			
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AUTHORS		Carninci,P., Shibata,Y., Hayatsu,N., Sugihara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.			
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JOURNAL		Genome Res. 10 (10), 1617-1630 (2000)			
MEDLINE		2049374			
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AUTHORS		Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Onodaki,Y., Muramatsu,M., Inoue,T., Kira,A. and Hayashizaki,Y.			
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JOURNAL		Genome Res. 10 (11), 1757-1771 (2000)			
MEDLINE		20530913			
PUBMED		11076861			
REFERENCE		4			
AUTHORS		Kawai,J., Shinaawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Haru,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,I., Sakai,K., Okido,T., Furuno,M., Aono,H., Balgarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,L., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyooka,K., Wang,K.H., Weitz,C., Whitaker,C., Wilmington,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaiji,H., Kohsuki,S. and Hayashizaki,Y.			
TITLE		Functional annotation of a full-length mouse cDNA collection			
JOURNAL		Nature 409 (6821), 685-690 (2001)			
MEDLINE		21085660			
PUBMED		11217851			
REFERENCE		5			
AUTHORS		The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.			
TITLE		Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs			
JOURNAL		Nature 420, 563-573 (2002)			
REFERENCE		6 (bases 1 to 4949)			
AUTHORS		Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,			





QY	1	MetaLaThrThrValThrCysThrArgPheThrAspGluTyrGlnLeuTyrGlnuAspIle	20
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VERSION BX420151.1 GI:30768004
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
```

```
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3877.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DF024C10P1&cluster=3877.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DF024C10P1.
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/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
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enriched, double-strand cDNA was digested with Not I and
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vector. Library was not normalized."
BASE COUNT 296 a 343 c 325 g 219 t 18 others
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Score: 1698.00 Matches: 340
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Best Local Similarity: 87.40% Mismatches: 16
Query Match: 62.54% Indels: 32
DB: 13 Gaps: 3
US-09-820-790B-2 (1-516) x BX420151 (1-1201)
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Db 84 ATGGCCACCACTGACCTGACCTGACCGCTTCCACGAGAGTACCACTACAGGATATT 143
Qy 21 GlyLysGlyAlaPheSerValValArgArgCysValLysLeuCysThrGlyHisGluTyr 40
Db 144 GGCAGAGGGGCTTCTCTGTGTGGTGGAGCTGTGTCAAGCTCTGCACCGGCAATGAGTAT 203
Qy 41 AlaAlaLysIleIleAsnThrLysLysLeuSerAlaArgAspHisGlnLysLeuGluArg 60
Db 204 SCAGCCAAAGATCATCAACACCAAGAGCTGTCCAGCCAGAGATCACCAAGCTGGAGAGA 263
Qy 61 GluAlaArgIleCysArgLeuLeuLysHisSerAsnIleValArgLeuHisAspSerIle 80
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Qy 81 SerGluGluGlyPheHisTyrLeuValPheAspLeuValThrGlyGlyGluLeuPheGlu 100
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Qy 101 AspIleValAlaArgGluTyrTyrSerGluAlaAspAlaSerHisCysIleGlnGlnIle 120
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Qy 141 AsnLeuLeuLeuAlaSerLysCysLysGlyAlaAlaValLysLeuAlaAspPheGlyLeu 160
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QY 301 LysGlyAlaIleLeuThrThrMetLeuAlaThrArgAsnPheSerValGlyArgGlnThr 320  
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QY 321 ThrAlaProAlaThrMetSerThrAlaAlaSerGlyThrThrMetGlyLeuValGluGln 340  
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RESULT 10  
 LOCUS AK032524 4207 bp mRNA linear HTC 05-DEC-2002  
 DEFINITION Mus musculus adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:6430579P05  
 product:calcium/calmodulin-dependent protein kinase II, delta, full insert sequence.

ACCESSION AK032524  
 VERSION AK032524.1 GI:26328338  
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 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1  
 AUTHORS Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636

REFERENCE 2  
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)  
 20499374  
 11042159

REFERENCE 3  
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, Y., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuda, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)  
 20530913  
 11076861

TITLE 4  
 JOURNAL Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Stauber, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wnshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409 (6821), 685-690 (2001)  
 21085660  
 11217851

TITLE 5  
 JOURNAL The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
 MEDLINE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 PUBMED Nature 420, 563-573 (2002)  
 REFERENCE 6 (bases 1 to 4207)  
 AUTHORS Adechi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akhiba, S., Takeda, Y., Tanaka, I., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site for further details.



## JOURNAL

Submitted (01-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

## REMARK COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [ccapbs-r@mail.nih.gov](mailto:ccapbs-r@mail.nih.gov)  
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 cDNA Library Preparation: Michael J. Brownstein (MGBRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)  
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www-shgc.stanford.edu>  
 Contact: (Dickson, Mark) [mcdépxil@stanford.edu](mailto:mcdépxil@stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILLNL at: <http://image.llnl.gov>  
 Series: TRAK Plate: 32 Row: d Column: 16  
 This clone has the following problem: frame shifted.

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 Best Local Similarity: 84.55% Mismatches: 29  
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US-09-820-790B-2 (1-516) x BC022558 (1-1374)

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 QY 241 ValThrProGluAlaLysAsnLeuIleAsnGlnMetLeuThrIleAsnProAlaLysArg 260  
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## RESULT 12

## AK081969

## LOCUS

## DEFINITION

## MUS MUSCULUS 16 DAYS EMBRYO HEAD CDNA, RIKEN FULL-LENGTH ENRICHED

## LIBRARY, CLONE: C130909G16 PRODUCT: CALCINUM/CALMODULIN-DEPENDENT

## PROTEIN KINASE II ISOFORM GAMMA-C PROTEIN KINASE II HOMOLOGY [Sus

## SCROFA], FULL INSERT SEQUENCE.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

AK081969 2132 bp mRNA linear HTC 05-DEC-2002  
 Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone: C130909G16 product: CALCINUM/CALMODULIN-DEPENDENT PROTEIN KINASE II ISOFORM GAMMA-C PROTEIN KINASE II HOMOLOGY [Sus scrofa], full insert sequence.

AK081969.1 GI:26100310

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

10349636

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL  
MEDLINE  
PUBLISHED  
REFERENCE  
AUTHORS

Genome Res. 10 (10), 1617-1630 (2000)  
20499374  
11042159

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akizawa, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, I., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,  
Okada, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
Yoneda, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer

TITLE

Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861

JOURNAL  
MEDLINE  
PUBLISHED  
REFERENCE  
AUTHORS

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,  
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,  
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamataka, I.,  
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, K.,  
Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,  
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,  
Kuehl, P., Lewis, S., Matsuo, Y., Nikaudo, I., Pesole, G.,  
Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, M., Tomita, M.,  
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,  
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,  
Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,  
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,  
Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,  
Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,  
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,  
Rato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H.,  
Toto, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L.,  
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kotsuki, S.,  
and Hayashizaki, Y.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409 (6821), 685-690 (2001)  
21085660  
11217851

TITLE

JOURNAL  
MEDLINE  
PUBLISHED  
REFERENCE  
AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 2132)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,  
Okazaki, Y., Saito, K., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Tagami, M., Togawa, A., Takahashi, F., Takaku-Akahira, S.,  
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
Muramatsu, M. and Hayashizaki, Y.

TITLE

JOURNAL  
MEDLINE  
PUBLISHED  
REFERENCE  
AUTHORS

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in RIKEN  
Genomic Sciences Center and Genome Science Laboratory in RIKEN  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/  
URL: http://fantom.gsc.riken.go.jp/.

FEATURES  
Location/Qualifiers  
Source

1. .2132  
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ISOFORM GAMMA-C PROTEIN KINASE II homolog [Sus scrofa]  
(SPTR1Q95263, evidence: FASTY, 100%ID, 100%length,  
match=1485)"

BASE COUNT 517 a 566 c 548 g 501 t

ORIGIN

Alignment Scores:  
Pred. No.: 1,31e-162 Length: 2132  
Score: 1601.00 Matches: 331  
Percent Similarity: 63.15% Conservative: 22  
Best Local Similarity: 59.21% Mismatches: 32  
Query Match: 58.97% Indels: 175  
DB: 11 Gaps: 4

US-09-820-790B-2 (1-516) x AK081969 (1-2132)

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Qy 41 AlaAlaLysIleIleAsnThrLysLysLysSerAlaArgAspHisGlnLysLeuGluArg 60

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Qy 61 GluAlaArgIleCysArgLeuLeuLysHisSerAsnIleValArgLysHisAspSerIle 80

Db 266 GAGGCCGGATATGCGGACTTCTGAACATCCAAACATTTGCGTCTCCATGACAGTATT 325

Qy 81 SerGluGluGlyPheHisTyrLeuValPheAspLeuValThrGlyGlyGluPheGlu 100

Db 326 TCTGAAGAGGGTTTCACTACCTCGTGTGTTGACCTGTGTACCGAGGGAGTTTGTGAA 385

Qy 101 AspIleValAlaArgGluTyrTyrSerGluAlaAspAlaSerHisCysIleGlnIle 120

Db 386 GACATTGTGCCAGAGAGTACTACAGTGAAGCTGATGCCAGCCACTGTATACATCAGATC 445

Qy 121 LeuGluAlaValLeuHisCysHisGlnMetGlyValValHisArgAspLeuLysProGlu 140

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Qy 141 AsnLeuLeuLeuAlaSerLysCysLysGlyAlaAlaValLysLeuAlaAspPheGlyLeu 160

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Qy 181 LeuSerProGluValLeuArgLysGluAlaTyrGlyLysProValAspIleTrpAlaCys 200

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 QY 373 -ProProAlaAlaLeuGluProGlnThrThrValIleHisAsnProValAspGlyIleLys 392  
 Db 1570 CTTGCAGACGCCATGAGCAACCAACCCCGTGGTACATATGATGATGATGATGATGATGATGAT 1629  
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 RESULT 13  
 BX445032  
 LOCUS

DEFINITION BX445032 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone  
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 ACCESSION BX445032  
 VERSION BX445032.1 GI:30778289  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1201)  
 AUTHORS Li, W.-B., Gruber, C., Jesse, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: segret@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 3877.r For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS1AF0062H1IOP1&cluster=3877.r. Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CS1AF0062H1IOP1.  
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 vector. Library was not normalized."  
 BASE COUNT 281 a 325 c 326 g 221 t 48 others  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 1,42e-161 Length: 1201  
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 Query Match: 58.49% Indels: 16  
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 QY 1 MetalThrValThrCysThrArgPheThrAspGluTyrGlnLeuTyrGluAspIle 20  
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|||||  
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Qy 221 LysLeuTyrGlnGlnIleLysAlaGlyAlaTyrAspPheProSerProGluTrpAspThr 240  
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Qy 301 LysGlyAlaIleLeuThrThrMetLeuAlaThrArgAsnPheSerValGly----- 317  
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ACCESSION AK044872  
VERSION AK044872.1 GI:26090581  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1  
AUTHORS Carninci, P. and Hayashizaki, Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636  
REFERENCE 2  
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itob, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
JOURNAL 20499374  
MEDLINE 11042159  
PUBMED 11042159  
REFERENCE 3  
AUTHORS Shibata, K., Itob, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
JOURNAL 20530913  
MEDLINE 11076861  
PUBMED 11076861  
REFERENCE 4  
AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, K., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojohori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staib, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Balzarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombauer, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409 (6821), 685-690 (2001)  
JOURNAL 21085660  
MEDLINE 11217851  
PUBMED 11217851  
REFERENCE 5  
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
JOURNAL 21085660  
MEDLINE 11217851  
PUBMED 11217851  
REFERENCE 6  
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koyas, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
Direct Submission  
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Tissues were provided by Dr. Tomohiro Kono (Department of Animal Science, Tokyo University of Agriculture, 1737 Hunko Atsugi City, Kanagawa Prefecture, Japan) whose assistance we gratefully acknowledge.  
Please visit our web site for further details.  
URL: <http://genome.gsc.riken.go.jp/>  
URL: <http://fantom.gsc.riken.go.jp/>

# FEATURES

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ORIGIN

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Best Local Similarity: 72.73% Mismatches: 15  
Query Match: 58.27% Indels: 83  
DB: 11 Gaps: 3

US-09-820-790B-2 (1-516) x AK044872 (1-2709)

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Db 852 TCATTGGCCAGTGTGCACCTTCAGTGGTCCATGAAGGCATGTGACCGACCTTGAGATT 911  
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Qy 162 eGluValGlnGlyAspGlnGlnAlaThrPheGlyPheAlaGlyThrProGlyTyrrLeuSe 182  
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DEFINITION CS02R033YN23 5-PRIME, mRNA sequence.  
ACCESSION BX420898  
VERSION BX420898.1 GI:30655024  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 934)  
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
CONTACT: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seq-ref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 3877.r For more information about this cluster, see

<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DF035CG120Pl&cluster=3877.r>. Contact : Feng Liang Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Paraday Avenue Genoscope sequence ID : CS0DF035CG120Pl.

## FEATURES

Location/Qualifiers

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BASE COUNT 207 a 282 c 264 g 176 t 5 others

## ORIGIN

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Pred. No.:	7.23e-156	Length:	934
Score:	1534.00	Matches:	289
Percent Similarity:	98.63%	Conservative:	0
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Query Match:	56.50%	Indels:	0
DB:	13	Gaps:	0

US-09-820-790B-2 (1-516) x BX420898 (1-934)

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QY	41	AlaAlaLysIleIleAsnThrLysLysLeuSerAlaArgAspHisGlnLysLeuGluArg	60
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DB	296	TCGAGAGGGGCTTCCACTACCTGGTCTCGATCTGGTCACTGGTGGGAGCTCTTTGAA	355
QY	101	AspIleValAlaArgGluTyrTyrSerGluAlaAspAlaSerHisCysIleGlnIle	120
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QY	121	LeuGluAlaValLeuHisCysHisGlnMetGlyValValHisArgAspLeuLysProGlu	140
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QY	241	ValThrProGluAlaLysAsnLeuIleAsnGlnMetLeuThrIleAsnProAlaLysArg	260
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QY	261	IleThrAlaHisGluAlaLeuLysHisProTrpValCysGlnArgSerThrValAlaSer	280
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Search completed: October 10, 2003, 10:54:15

Job time : 3241 secs

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Qy	476	IleAspGlyGlnGlyArgProArgThrSerGlnSerGluGluThrArgValTrpHisArg	495	
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; APPLICANT: Immunex Corporation				
; APPLICANT: Bird, Timothy A.				
; APPLICANT: Virca, G. Duke				
; APPLICANT: Martin, Unja				
; APPLICANT: Anderson, Dirk M.				
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES				
; FILE REFERENCE: 2923-A				
; CURRENT APPLICATION NUMBER: US/09/579,664B				
; CURRENT FILING DATE: 2000-05-26				
; NUMBER OF SEQ ID NOS: 36				
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QY	154	LysLeuAlaAspPheGlyLeuAlaIleGluValGlnValAspGlnGlnAlaTrpPheGly	173
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Db	963	GATTCCTCCCTACTGGGATGACATCTCGACTCTGCCAAGACTCATTCGGAACTGATG	1022
QY	254	ThrIleAsnProAlaLysArgIleThrAlaHisGluAlaLeuLysHisProTrpValCys	273
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Db	1143	TTTGCAAAAGACCAATGAGACACAGGTTTAAAGCCAGCGAGTCGTGAGACATATCGGG	1202
QY	302	GlyAlaIleLeuThrThrMetLeuAlaThrArgAsnPheSerValGlyArgGlnThrThr	321
Db	1203	AGGTCACGCTGGCAGCAGCGCTGGACAGTTCAATGCAAGTGTCTCTCACCAACCTCAGT	1262
QY	322	AlaProAlaThrMetSerThrAlaAlaSerGlyThr	333
Db	1263	TTG---GCCAGCCAAAAGATGTGGCTGTGGCAC	1295

### RESULT 3

RESULT 3  
PS-09-620-312D-526

US-09-020-312D-320  
: Sequence 526, Application US/09620312D

: Sequence 326, Appl  
: Patent No. 6569662

; FACSIMIL NO. 05090002  
; GENERAL INFORMATION:



```

Db      2119 CAAGACAGCGCGCGCTGGGATGGAGCCCATCTCTCCAGTTCCTCCCTCAGTGGAGGAG 2178
QY      342 sSerLeuLeuAsnLysLysAlaAspGlyValLysProGlnThrAsnSerThrLysAsnSe 362
Db      2179 AFCCCTGTGGCTGGGAGAGCAGTCCCGGCCGCCACCCCTCCCGAAT-----2224
QY      362 rAlaAlaAlaThrSerProLysGlyThrLeuProProAlaAlaLeuGluProGlnThr 382
Db      2225 -----CTCCACCCGCCCACTGTCTCCCGCTCCCGCG 2256
QY      382 rValLeuHisAsnProValAspGly 390
Db      2257 GGTGGTGAGCGGGCAGGAACCTGGC 2281

RESULT 5
US-09-975-326-1
; Sequence 1, Application US/09975326
; Patent No. 6476210
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. 6476210el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0254-USA
; CURRENT APPLICATION NUMBER: US/09/975,326
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/239,821
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2301
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-975-326-1

Alignment Scores:
Pred. No.:      7 19e-54      Length:      2301
Score:          586.50      Matches:      139
Percent Similarity: 53.47%      Conservative: 69
Best Local Similarity: 35.73%      Mismatches: 153
Query Match:      21.60%      Indels:      28
DB:              4          Gaps:      7

US-09-820-790B-2 (1-516) x US-09-975-326-1 (1-2301)
QY      12 AspGluThrGlnLeuThrGluAspGlyGlyAlaPheSerValValArgCys 31
Db      1174 GAGAAATACAAATTTGAAAGGATGATGGTATGCGCAATTTTCAGTAGTCAAGAGTGT 1233
QY      32 ValLysLeuCysThrGlyHisGluThrAlaAlaLysLeuLeuAsnThrLysLysLeuSer 51
Db      1234 ATAGACAGGTCCATCGAAGGAGGATGTCCTTAAAGATTATAGACAAAGCCCAATGTGT 1293
QY      52 AlaArgAspHisGlnLysLeuGluArgGluAlaAlaArgLeuCysArgLeuLysHisSer 71
Db      1294 GGAAGAAAGAACAC---CTGATTGAGATGAAGTGTCAATACTACTGCGCGAGTGAACATCCC 1350
QY      72 AsnLeuValArgLeuHisAspSerLeuSerGluGluGlyPheHisThrLeuValPheAsp 91
Db      1351 AATATCATATTGCTGGTCGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1410
QY      92 LeuValThrGlyGlyGluLeuPheGluAspLeuValAlaArgGluThrThrSerGluAla 111
Db      1411 TTGGTCAAAAGGTGGAGATCTCTTTGATGCAATTAATCTCGTCCGACCAAGTACACTGAGAGA 1470
QY      112 AspAlaSerHisCysLeuGlnLeuGlnLeuGluAlaValLeuHisCysHisGlnMetCly 131
Db      1471 GATGGCAGTGCCATGGTGTACAACTTAGCCATGCCCTCAGGTATCTCCATGGCCTCAGC 1530
QY      132 ValValHisArgAspGluLysProGluAsnLeuLeuAlaSerLysCysLysAla 151
Db      1531 ATCGTGCACAGACATCAACACCGAGAGATCTCTGTGTGTGAATATCTCGATGCGAACCC 1590

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QY      152 ---AlaValLysLeuAlaAspPheGlyLeuAlaIleGluValGlnGlyAspGlnGlnAla 170
Db      1591 AAGTCTTTTGAAGCTGGGAGACTTTGGCTTGGACTGTGGTAGAAGGC-----CCT 1641
QY      171 TrpPheGlyPheAlaGlyThrProGlyThrLeuSerProGluValLeuArgLysGluAla 190
Db      1642 TTATACACAGCTGTGGGCACACCATTTATGGTGTCCAGAAATCAFTGCTGAACCTGGC 1701
QY      191 TyrGlyLysProValAspLeuPheAlaCysGlyValIleLeuThrIleLeuValGly 210
Db      1702 TATGGCCTGAAGTGTGACATTTGGCAGCTGTGTGTGATACATACATACATCTCTGTGGA 1761
QY      211 TyrProPheThrPaspGluAsp-----GlnHisLysLeuThrGlnGlnIleLysAla 228
Db      1762 TTCCACCATCTCCGAAGTGAGACAATCTCCAGGAAGATCTCTTCGACCACTCTTGCT 1821
QY      229 GlyAlaTyrAspPheProSerProGluThrPaspThrValThrProGluAlaLysAsnLeu 248
Db      1822 GGGAGCTGTGGATTTCCGGCCCCCTACTGGGATACATCAGGACTCTGCCAAGGATTA 1881
QY      249 IleAsnGlnMetLeuThrIleAsnProAlaLysArgIleThrAlaHisGluAlaLys 268
Db      1882 ATCAGTCAATGCTTCAGGTAATGTGAAGCTCGGTGTACCGCGGACAAATCTGTGAGT 1941
QY      269 HisProThrValCysGlnArgSerThrValAlaSerMetMetHisArgGlnGluThrVal 288
Db      1942 CACCCCTGGTGTGAGATGATGCTCCAGGAGATACATCAGAGCTGAGGTGACAGGT 2001
QY      289 GluCysLeuLysLysPheAsnAlaArgLysLeuLysGlyAlaIleLeuThrThrMet 308
Db      2002 AAACATAAACAGCAGCACTTTAATATGCGCTCCCAAGAACAGACAGCACTACCACCGGGTC 2061
QY      309 LeuAlaThrArgAsnPheSerValGlyArg-----GlnThr-ThrAlaProAlaThrMe 326
Db      2062 TCCGTCTATCATGAACACAGCTCTAGATAGGAGGCGAGATTTCTCGACCAAGCACTGT 2121
QY      326 tSerThrAlaAla-----SerGlyThrThrMetGlyLeuValGluGlnAlaLys 342
Db      2122 CAAGACAGCGGCGAGCGCTGGGATGGAGCCCATCTCTCCAGTTCCTCCCTCAGTGGAGGAG 2181
QY      342 sSerLeuLeuAsnLysLysAlaAspGlyValLysProGlnThrAsnSerThrLysAsnSe 362
Db      2182 ATCCCTGTGCTGGGAGAGCAGTCCCGGCCCCACCCCTCCGGAAT-----2227
QY      362 rAlaAlaAlaThrSerProLysGlyThrLeuProProAlaAlaLeuGluProGlnThr 382
Db      2228 -----CTCCACCCCGCCACTGTCTCCCGCTGCCCG 2259
QY      382 rValIleHisAsnProValAspGly 390
Db      2260 GGTGGTGAGCGGGCAGGAACCTGGC 2284

RESULT 6
US-09-016-434-1454
; Sequence 1454, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 843-4166
; INFORMATION FOR SEQ ID NO: 1454:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1480 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g790789
; US-09-016-434-1454

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Alignment Scores:
Pred. No.: 5,74e-54 Length: 1480
Score: 584.50 Matches: 150
Percent Similarity: 53.28% Conservative: 61
Best Local Similarity: 37.88% Mismatches: 138
Query Match: 21.53% Indels: 48
DB: 4 Gaps: 12

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US-09-820-790b-2 (1-516) x US-09-016-434-1454 (1-1480)

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QY 12 AspGluTrpGlnLeuTyrGluAspIleGlyLysGlyAlaPheSerValVal-----28
DB 199 GACATCTACGACTCCGAGATTCCTGGCAGCGGGGCTTCTCGAGGTGATCTCTGGCA 258
QY 29 -----ArgArgCysValLysLeuCysThrGlyHisLysLysAlaAlaLysIleLeu 46
DB 259 GAAGATGAAGAGGACGCAAGAGCTG-----GTGGCCATCAATGATCTGCTGCC 303
QY 47 ThrLysLysLeuSerAlaAspHisGlnLysLeuGluArgGluAlaArgIleCysArg 66
DB 304 AAGGAGGCCCTGGAGGCAAGGAA---GGCAGCATGGAGATGAGATTGCTGCTGCCAC 360
QY 67 LeuLeuLysHisSerAsnIleValArgLeuHisAspSerIleSerGluGluGlyPheHis 86
DB 361 AAGATCAAGACCCCAACATTTGAGCCCTG---GATGACATCTATGAGATGGGGGCCAC 417
QY 87 ---TyrLeuValPheAspLeuValThrGlyGlyGluLeuPheGluAspIleValAlaArg 105
DB 418 CTCATCTCATCTATGACGTGTCTGGGTGGGAGCTCTTTGACCGTATGTGGAAAA 477
QY 106 GluTyrTyrSerGluAlaAspAlaSerHisCysIleGlnIleLeuGluAlaValLeu 125
DB 478 GGCCTTACACGAGCGGAGCCAGCCGCTCATCTCCAGGTGCTGATGCTGTGAA 537
QY 126 HisCysHisGlnMetGlyValValHisArgAspLeuLysProGluAsnLeuLeuAla 145
DB 538 TACTGTGATGACCTGGGCTATGTACCGGATCTCAAGCAGAGATCTGCTGTACTAC 597
QY 146 SerLysCysLysGlyAlaAlaValLysLeuAlaAspPheGlyLeuAlaIleGluValGln 165
DB 598 AGCCTGATGAGACTCCAAATCATGATCTCCGACTTTGGCTCTCC---AAGATGGAG 654
QY 166 GlyAspGlnGlnAlaTrpPheGlyPheAlaClyThrProGlyTyrLeuSerProGluVal 185
DB 655 GACCGGGGAGTGTGCTCTCCACCGCTGTGAAGATCCGGGATAGTGGCCCTGAATC 714

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QY 186 LeuArgLysGluAlaValTyrGlyLysProValAspIleTrpAlaCysGlyValIleuTyr 205
DB 715 CTGGCCAGAGCCCTACAGAGGCTGTGATTTGCTGTGTCATAGGTGATCGCTAC 774
QY 206 IleLeuLeuValGlyTyrProPheTrpAspGluAspGlnHisLysLysLeuTyrGlnGln 225
DB 775 ATCTTGCTCTCGGTTACCTCCCTTCTATGACAGATGATGCCAACTCTTTGACAG 834
QY 226 IleLysAlaGlyAlaTyrAspPheProSerProGluTrpAspThrValThrProGluAla 245
DB 835 ATTTTGAAGCGCGAGTAGTACAGTTTACTCTCTTACTGGGACGACATCTGACTCTGC 894
QY 246 LysAsnLeuIleAsnGlnMetLeuThrIleAsnProAlaLysArgIleThrAlaHisGln 265
DB 895 AAGATTTTCATCCGGCACTTGATGGAGAGGACCCAGAGAAAGATTCACCTGTGGCAG 954
QY 266 AlaLeuLysHisProTrpValCysGlnArgSerThrValAlaSerMetMetHisArgGln 295
DB 955 GCGTTGCAGACCCCATGGATTGCGAGGATACAGCTCTAGATAGAAATATCCAC---CAG 1011
QY 286 GluThrValGluCysLeuLysLysPheAsnAlaArgLysLeuLysGlyAlaIleLeu 305
DB 1012 TCGGTGAGTGAGCAGATCAGAGAACTTTCGCAAGAGCAGTGGAGCAGACCTTCAAT 1071
QY 306 ThrThrMetLeuAlaThrArgAsnPheSerValGlyArgGlnThrThrAlaProAlaThr 325
DB 1072 GCCAGCGCTGTGTGGCGCACATGAGAACTGCGAGTGGCGCACCGACCGAGGAGCG 1131
QY 326 MetSerThrAlaAlaSerGlyThrThrMetGlyLeuValGluGlnAlaLysSerLeuLeu 345
DB 1132 GGCAGACGCGGAGCCATGGG-----GAGCTGCTG 1161
QY 346 AsnLysLysAlaAspGly-----ValLysPro 354
DB 1162 ACACCAAGTGGTGGGGCGCGCAGCTGTGCTGTGAGACATGCTGTGGAGCG 1221
QY 355 GlnThrAsnSerThrLysAsnSerAlaAlaThrSerProLysGlyThrLeuProPro 374
DB 1222 GGCACAGAA-----CTGTCCCCC-----ACACTGCC-CCA 1250
QY 375 AlaAlaGluLeuProGlnThrThrValIleHisAsnProValAspGly 390
DB 1251 CCAGCTCTAGGCCCCCTGGACCTGGGT---CATGATCTCTGCTGGTGG 1295

```

# RESULT 7

```

; US-09-620-312D-809
; Sequence 809, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyun
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunging
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317

```

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1  RESULT 8
2  US-08-715-568A-2
3  ; Sequence 2, Application US/08715568A
4  ; Patent No. 5856463
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Prydz, Hans Peter Blankenberg
7  ; APPLICANT: Bræde, Gaute
8  ; TITLE OF INVENTION: PSKH-1 Ribozymes and Uses in Disease
9  ; TITLE OF INVENTION: Treatment
10 ; NUMBER OF SEQUENCES: 14
11 ; CORRESPONDENCE ADDRESS:
12 ; ADDRESSER: Lerner, David, Littenberg, Krumholz & Mentlik
13 ; STREET: 600 South Avenue West
14 ; CITY: Westfield
15 ; STATE: NJ
16 ; COUNTRY: USA
17 ; ZIP: 07090-1497
18 ; COMPUTER READABLE FORM:
19 ; MEDIUM TYPE: Floppy disk
20 ; COMPUTER: IBM PC compatible
21 ; OPERATING SYSTEM: PC-DOS/MS-DOS
22 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
23 ; CURRENT APPLICATION DATA:
24 ; APPLICATION NUMBER: US/08/715.568A
25 ; FILING DATE:
26 ; CLASSIFICATION: 514
27 ; ATTORNEY/AGENT INFORMATION:
28 ; NAME: Foley, Shawn P.
29 ; REFERENCE/DOCKET NUMBER: FORSK 3.0-002
30 ; TELECOMMUNICATION INFORMATION:
31 ; TELEPHONE: 908-654-5000
32 ; TELEFAX: 908-654-7866
33 ; INFORMATION FOR SEQ ID NO: 2:
34 ; SEQUENCE CHARACTERISTICS:
35 ; LENGTH: 3471 base pairs
36 ; TYPE: nucleic acid
37 ; STRANDEDNESS: double
38 ; TOPOLOGY: linear

```

[illegible]



Db 496 TTTATCTCTCTGAGTGGCCACGGGGAGGGGTTTGACTGGATCCTGGACCGAGGC 555  
 QY 107 TTTATCTCTCTGAGTGGCCACGGGGAGGGGTTTGACTGGATCCTGGACCGAGGC 555  
 Db 556 TACTATCTCTGAGTGGCCACGGGGAGGGGTTTGACTGGATCCTGGACCGAGGC 555  
 QY 127 CysHisMetGlyValValHisArgAspLeuLysProGluAsnLeuLeuAlaSer 146  
 Db 616 TTGCATCTCTGAGTGGCCACGGGGAGGGGTTTGACTGGATCCTGGACCGAGGC 555  
 QY 147 LysCysLysGlyAlaValLysLeuAlaAspPheGlyLeuAlaIleGluValGlnGly 166  
 Db 676 CGGTGAGAGTCTGAGTGGCCACGGGGAGGGGTTTGACTGGATCCTGGACCGAGGC 555  
 QY 167 AspGlnGlnAlaThrPheGlyPheAlaGlyThrProGlyLysLeuSerProGluValLeu 186  
 Db 736 CTCTCAAGGAG-----CCCTGTGGAGCCCGAGTATCTGGCCACGAGAGGTGA 786  
 QY 187 ArgLysGluAlaThrGlyLysProValAspIleThrAlaCysGlyValIleLeuTyrlle 206  
 Db 787 GCGCGGAGCGGTATGGAGCGCTGTGGACTCTGGCCATGGAGTATCATCATGATCATC 846  
 QY 207 LeuLeuValGlyThrProPheThrAspGlu-----AspGlnHis 220  
 Db 847 CTGCTTTTCAGGCAATCCACCTTCTATGAGGAGGTGGAAGAGATGATTATGAGAACCAT 906  
 QY 221 -----LysLeuTyrlleGlnIleLysAlaGlyAlaTyrlleAspPheProGluThr 238  
 Db 907 GATGAGAACTCTTCGCAAGTCTCTGGTGGTATGATGATGATGATGATGATGATGATG 966  
 QY 239 AspThrValThrProGluAlaLysLeuAlaAsnGlnMetLeuThrIleAsnProAla 258  
 Db 967 GATGATATTTTCGAGGAGCCCAAGACCTGGTCAAGGCTGATGAGGTGGAGCAAGAC 1026  
 QY 259 LysArgIleThrAlaHisGluAlaLeuLysHisProThrValCysGlnArgSerThrVal 278  
 Db 1027 CAGCGGATCATCTCAGAGAGGCGCATCTCCATGATGATGATGATGATGATGATGATG 1080  
 QY 279 AlaSerMetMetHisArgGlnGluThrValGluCys-----LeuLysLysPheAsnAla 296  
 Db 1081 CCTTCTGATGAGACATCATGAGTGGTGTCT-----TGTCGCCAGATTTGAAGAAGCTTGGC 1137  
 QY 297 ArgArgLysLeuLysGlyAlaIleLeuThrThrMetLeuAlaThrArgAsnPheSerVal 316  
 Db 1138 AGGCGCAAGTGGAGAGGCTCTCGAGTGCACCCCTCATGAAAGCGCTCCGGGACCA 1197  
 QY 317 GlyArgGlnThrThrAlaProAlaThrMetSerThr-----TCTGGCAATGCT 1257  
 Db 1198 GAGCAGTCCAGCAGCGCTCGAGCCAGTGGGCTCTGAGCCAGACAGACTGCCCCCGGG 1257  
 QY 329 AlaAlaSerGlyThrThrMetGlyLeuValGlnGlnAlaLysSerLeuLeuAsn----- 346  
 Db 1258 GCTCAGGTGGGCGCACAGCTCGAGTGGAGTGGAGTACCTCAGCCCTGAGGTGAT 1317  
 QY 347 -----LysLysAlaAspGlyValLysProGlnThrAsnSer-----Thr 359  
 Db 1318 GCTCCTGCTCTCAAGAGTGAATGTGGCCCGCCAGACCGTAGTGGCCACCCAGCC 1377  
 QY 360 LysAsnSerAlaAlaAlaThrSerProLysGlyThrLeuProProAla-----Ala 376  
 Db 1378 ACAGTGAAGTGGCCAGCCAGCCAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 1437  
 QY 377 LeuGluProGlnThrThrValIleHisAsnProValAspGlyIleLysGluSerSerAsp 396  
 Db 1438 ATCACTCCAGCCACTGATGGAGTGTACCCAGTCT-----ACTGACAGG 1482  
 QY 397 SerAlaAsnThrThrThrLeuAspGluAspAlaLysAlaArgLysGlnGluIleLys 416  
 Db 1483 AGCGCTACTCCAGCCACTGATGGAGAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAG 1542  
 QY 417 ThrThrGluGlnLeuIleGluAlaValAsnGlnLysPheGluAlaTyrlleAlaPheTyrl 436

Db 1543 ACCACCCAAAGCAGTGGCCATGCTGGCCACCAAGGCA-----GCTGCCACC 1587  
 QY 437 PheGluAsnLeuLeuAlaLys-----AsnSerLysProIleHisThrThrIleLeuAsn 454  
 Db 1588 CTTGAGCGGCTATGGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGGCT 1647  
 QY 455 ProHisValHisValIleGlyLysAspAlaAlaCysIleAlaTyrlleArgLeuThrGln 474  
 Db 1648 CCACCTCTAGTAATA-----GGGAGAGGCTGCT----- 1677  
 QY 475 TyrIleAspGlyGlnGlyArgProArgThrSerGlnSerGlnGluThr----- 490  
 Db 1678 -----GGTATGCCAGGAGTCTCAAGAGGAGGAGCCAGCTGAGTAGGC 1722  
 QY 491 -----ArgValThrHisArgArgAspGlyLysThrProGlnAsn----- 502  
 Db 1723 AGCCTGCTGAGGGGGGCGAGGGGATG-----GCAGGAGGTGGAGAGTGGATGA 1773  
 QY 503 -----ValHisPheHisCysSerGlyAlaProValAlaPro 514  
 Db 1774 GGGGCTTCTCACTGTACATGAGTGCATGCGCATGATGCGCTGCCCATGCCCC 1830  
 RESULT 10  
 US-09-620-312D-20  
 ; Sequence 20, Application US/09620312D  
 ; Patent No. 6569662  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tang, Y. Tom  
 ; APPLICANT: Liu, Chenghua  
 ; APPLICANT: Asundi, Vinod  
 ; APPLICANT: Zhang, Jie  
 ; APPLICANT: Ren, Feiyang  
 ; APPLICANT: Chen, Rui-hong  
 ; APPLICANT: Zhao, Qing A.  
 ; APPLICANT: Wehrman, Tom  
 ; APPLICANT: Xue, Aidong J.  
 ; APPLICANT: Yang, Yonghong  
 ; APPLICANT: Wang, Jian-Rui  
 ; APPLICANT: Zhou, Ping  
 ; APPLICANT: Ma, Tunding  
 ; APPLICANT: Wang, Dunrui  
 ; APPLICANT: Wang, Zhiwei  
 ; APPLICANT: John Tillinghast  
 ; APPLICANT: Dmanac, Radoje T.  
 ; TITLE OF INVENTION: No. 6569662el Nucleic Acids and  
 ; FILE REFERENCE: 784CIP2B  
 ; CURRENT APPLICATION NUMBER: US/09/620,312D  
 ; CURRENT FILING DATE: 2000-07-19  
 ; PRIOR APPLICATION NUMBER: 09/552,317  
 ; PRIOR FILING DATE: 2000-04-25  
 ; PRIOR APPLICATION NUMBER: 09/488,725  
 ; PRIOR FILING DATE: 2000-01-21  
 ; NUMBER OF SEQ. ID NOS: 1105  
 ; SOFTWARE: pc\_Fl\_genes Version 1.0  
 ; SEQ ID NO 20  
 ; LENGTH: 2840  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (206)..(1711)  
 US-09-620-312D-20  
 Alignment Scores:  
 Pred. No.: 2,738-49 Length: 2840  
 Score: 546.00 Matches: 170  
 Percent Similarity: 47.59% Conservative: 97  
 Best Local Similarity: 30.30% Mismatches: 196  
 Query Match: 20.11% Indels: 98  
 DB: 4 Gaps: 22  
 US-09-820-790B-2 (1-516) x US-09-620-312D-20 (1-2840)

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QY 11 ThrAspGluTyrGlnLeuTyrGlnAspIleGlyLysGlyAlaPheSerValValArgArg 30
Db 266 ACTGACAGATATGATTTGGACAGGTCATCAAGACTGAGGAGTTTGTGAATCTTCCGG 325
QY 31 CysValLysLeuCysThrGlyHisGluTyrAlaAlaLysLeuLeuAsnThrLysLysLeu 50
Db 326 GCCAAGGCAAGACAGCAGC-----AAGCTGCACACCTGTCAGAGAGTTC 370
QY 51 SerAlaArgAspHisGlnLysLeuGluArgGluAlaArg-----IleCysArg 66
Db 371 CAGAACGGGACGGCCGACAGGTGCGGAAGCTGCCAAGAACGAGATAGCATCTCAG 430
QY 67 LeuLeuLysHisSerAsnIleValArgLeuHisAspSerIleSerGluGluGlyPheHis 86
Db 431 ATGGTGAACATCCACATCCTACAGCTGTGGATGTTGTGTGACCCGCAAGAGTAC 490
QY 87 TyrLeuValPheAspLeuValThrGlyGlyGluLeuPheGluAspIleValAlaArgGlu 106
Db 491 TTTATCTTCTCGAGCTGGCCAGCGGAGGAGGTGTTGACTGGATCCTGGACCAAGGGC 550
QY 107 TyrTyrSerGluAlaAspAlaSerHisCysIleGlnGlnIleLeuGluAlaValLeuHis 126
Db 551 TACTACTCGGACGAGACACAGCAACAGTGTACGCAAGTCTGTGGAGCCGTGCCAT 610
QY 127 CysHisGlnMetGlyValValHisArgAspLeuLysProGluAsnLeuLeuAlaSer 146
Db 611 TTGCATCTACTCAAGATCTGCACAGGAATCTCAAGCTGGAGAACCTGGTTACTACAC 670
QY 147 LysCysLysGlyAlaAlaValLysLeuAlaAspPheGlyLeuAlaIleGluValGlnGly 166
Db 671 CGGCTGAGAACTCGAAGATGTTTCATCAGTGACTTCCATCTGGCTAAGCTAGAAATGGC 730
QY 167 AspGlnGlnAlaThrPheGlyPheAlaGlyThrProGlyTyrLeuSerProGluValLeu 186
Db 731 CTGATCAAGAG-----CCGTGTGGACCCCGAGTATCTGGCCCGACAGAGTGTA 781
QY 187 ArgLysGluAlaTyrGlyLysProValAspIleTyrPalaCysGlyValIleLeuTyrIle 206
Db 782 GGCGGACGCGTATGAGGCGCCGTGTGGACTGCTGGCCATTGGAGTTCATGATGATC 841
QY 207 LeuLeuValGlyTyrProProPheTrpAspGlu-----AspGlnHis 220
Db 842 CTGCTTTCAGGAATCCACCTTCTATGAGGAGGTGGAAGAGATGATTATGAGACCAT 901
QY 221 -----LysLeuTyrGlnGlnIleLysAlaGlyValTyrAspPheProSerProGluTrp 238
Db 902 GATAAGAACTCTTCCGCAAGATCCGTGGTGGTACTATGATTTGACTCTCCATATGG 961
QY 239 AspThrValThrProGluAlaLysAsnLeuLeuAsnGlnMetLeuThrIleAsnProAla 258
Db 962 GATGATATTTCGACGACGACCAAGACCTGGTCACAGGCTGATGGAGGTGGAGCAAGAC 1021
QY 259 LysArgIleThrAlaHisGluAlaLeuLysHisProTyrValCysGlnArgSerThrVal 278
Db 1022 CAGCGGATCTGCGAGAGAGGCGCATCTCCATGAGTGAT-----TCTGGCAATGCT 1075
QY 279 AlaSerMetHisArgGlnGlnThrValGluCys-----LeuLysLysPheAsnAla 296
Db 1076 GCTTCTGATAAAGAACATCAAGATGTGTGTC---TGTGCCAGATTTGAAAGAACTTTGCC 1132
QY 297 ArgArgLysLysGlyAlaIleLeuThrMetLeuAlaThrArgAsnPheSerVal 316
Db 1133 AGGCGCAAGTGGGAAGAGCGCTGCGAGTGACCCCTCATGAACGGCTCGCGGGCAACA 1192
QY 317 GlyArgGlnThrThrAlaProAlaThrMetSerThr----- 328
Db 1193 GAGCAGTCCAGCAGCGCTGACGCCAGTCCGCTCAGCCACAGACACTGCCACCCCGGG 1252
QY 329 AlaIaSerGlyThrThrMetGlyLeuValGluGlnAlaLysSerLeuLeuAsn----- 346
Db 1253 GCTGCAAGTGGGCCACAGCTGCAGCTGCAGTGGAGCTACCTACGACCCCTGAGGGTGT 1312
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QY 347 -----LysLysAlaAspGlyValLysProGlnThrAsnSer-----Thr 359
Db 1313 GGTGCTGCTGCTCCAAAGAGTGAATAATGTGCCCCCGCCAGACCGTAGTGCACCCAGCC 1372
QY 360 LysAsnSerAlaAlaAlaThrSerProLysGlyThrLeuProProAla-----Ala 376
Db 1373 ACAGATGGAATGCCACCCAGCCACTGATGGCAGTGTCCACCCAGCCACCGTAGGAGAC 1432
QY 377 LeuGluProGlnThrThrValIleHisAsnProValAspGly-----IleLysGluSerSer 395
Db 1433 ATCACTCCAGCCACT-----GATGGAGTGTCCACCCAGCCACT 1471
QY 396 AspSerAlaAsnThrThrIleGluAspGluAspAla-----LysAlaArgLysGlnGluIle 414
Db 1472 GACAGGAGCGCTACTCCATCCACTGATGGATAGCCACACCCAGCCACAGAGAGCACT 1531
QY 415 IleLysThrThrGluGlnLeuIleGluAlaValAsnAsnGlyAspPheGluAlaTyrAla 434
Db 1532 GTGCCCCACCCCAAGCAGTCCCATGTGCGCCACCAAGGCA-----GCT 1576
QY 435 PheTyrPheGluAsnLeuLeuAlaLys-----AsnSerLysProIleHisThrThrIle 452
Db 1577 GCCACCCCTGAGCGGCTATGGCCAGCCGACAGACACACCCAGAGGGCGGCCAGAGCC 1636
QY 453 LeuAsnProHisValHisValIleGlyGluAspAlaAlaCysIleAlaTyrIleArgLeu 472
Db 1637 CAGGCTCCACCTCTAGTAAA---GGGAGAGAGCTGCT----- 1672
QY 473 ThrGlnTyrIleAspGlyGlnGlyArgProArgThrSerGlnSerGluGluThr----- 490
Db 1673 -----GGTTATGCCAGAGAGTCTCAAGGGAGGAGGCGCCAGCTGA 1711
QY 491 -----ArgValTrpHisArgArgAspGlyLysTrpGlnAsn 502
Db 1712 GTAGCAGCCTGTGTGGGGGGGCGAGGGATGG-----GCAGGAGGTGGAGAGT 1762
QY 503 -----ValHisPheHisCysSerGlyAlaProValAla 513
Db 1763 GGATGAGGGGCTTCTCACTGTATACATAGAGTCACTGGCATGATGCGCTCCCGCATGC 1822
QY 514 Pro 514
Db 1823 CCC 1825
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RESULT 11  
US-09-620-312D-19  
; Sequence 19, Application US/09620312D  
; Patent No. 6569662  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Wang, Yonghong  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Zhou, Ping  
; APPLICANT: Ma, Yuxing  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: John Tillinghast  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and  
; FILE REFERENCE: 784CIP2B  
; CURRENT APPLICATION NUMBER: US/09/620,312D  
; CURRENT FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 09/552,317  
; PRIOR FILING DATE: 2000-04-25



APPLICANT: Shah, Purvi  
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN  
NUMBER OF INVENTION: KINASES  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/878,989  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0321 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:

## INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1282 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: PROSNOT06  
CLONE: 827431  
US-08-878-989-12

## Alignment Scores:

Pred. No.: 1,77e-49 Length: 1282  
Score: 542.50 Matches: 112  
Percent Similarity: 61.15% Conservative: 47  
Best Local Similarity: 43.08% Mismatches: 96  
Query Match: 19.98% Indels: 5  
DB: 2 Gaps: 4

US-09-820-790B-2 (1-516) x US-08-878-989-12 (1-1282)

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Db 243 TACGAGATCCGAGAGGCTCGGTCGCTTCCGAGGTGGTCTGCGCCAGGAG 302  
Qy 34 LeuCysThrGlyHisGluTyrAlaAlaIleAlaSerThrLysLeuSerAlaArg 53  
Db 303 CGGGCTCCGACACCTCGTGGCCCTCAAGTGCATCCCAAGAGGCGCTCGGGGCAAG 362  
Qy 54 AspHisGlnLysLeuGluArgGluAlaArgIleCysArgLeuLeuLysHisSerAsnIle 73  
Db 363 GAG---GCCCTGGTGAGAACGATCGAGTGCCTCGTAGGATCAGTCAACCCACATC 419  
Qy 74 ValArgLeuHisAspSerIleSerGluGlyPheHisTyrLeuValPheAspLeuVal 93  
Db 420 GTCGCTCGGAGGATGCCACGAGAGCCCTCCACCTCTACCTGGCCATGACTGGTG 479  
Qy 94 ThrGlyGlyGluLeuPheGluAspIleValAlaArgGluTyrTyrSerGluAlaAspAla 113  
Db 480 ACGGTGGCGAGCTGTTACCGGCATCATGAGCGGGCTCTACACAGAGAGGATGCC 539  
Qy 114 SerHisCysIleGlnGlnIleLeuGluAlaValLeuHisCysHisGlnMetGlyValVal 133

Db 540 AGCCATCTGTGGTCTCAGTCTTGGCCCTCTCCCTACCTGCACAGCTGGGATCGT 599  
Qy 134 HisArgAspLeuLysProGluAsnLeuLeuLeuLeuLysCysLysGlyAlaAlaVal 153  
Db 600 CACCGGAGCTCAGCCCGAAGACCTCTGTATGCCACGCCCTTTGAGGACTCGAAGATC 659  
Qy 154 LysLeuAlaAspPheGlyLeuAlaIleGluValGlnGlyAspGlnGlnAlaTrpPheGly 173  
Db 660 ATGGTCTCTGACTTTGGACTCTCC---AAAATCCAGGCTGGGAACATG-----CTAGGC 710  
Qy 174 PheAla---GlyThrProGlyTyrLeuSerProGluValLeuArgLysGluAlaTyrGly 192  
Db 711 ACGCCTGTGGACCCCTCGATATGTGCCCCAGAGCTCTGGAGCAGAACCCCTAGGG 770  
Qy 193 LysProValAspIleTrpAlaCysGlyValIleLeuTyrIleLeuLeuValGlyTyrPro 212  
Db 771 AAGCCGTAGATGTGTGGCCCTGGGCTCATCTCCATCTCTACATCTCTGTGTGGTACCCC 830  
Qy 213 ProPheTrpAspGluAspGlnHisLysLeuTyrGlnGlnIleLysAlaGlyAlaTyrAsp 232  
Db 831 CCTTCTACGACGAGACGCCCTGAGCTCTGAGCCAGATCTCTGAGGCGCCAGCTATGAG 890  
Qy 233 PheProSerProGluTrpAspThrValThrProGluAlaLysAsnLeuLeuMet 252  
Db 891 TTGACTNTCTCTTCTGGGATGACATCTCAGAAATCAGGCAAGACTTTATTTCGCACCTT 950  
Qy 253 LeuThrIleAsnProAlaLysArgIleThrAlaHisGluAlaLeuLysHisProTyrVal 272  
Db 951 CTGGAGCGGAGACCTTCAGAGAGGTTACCTGCCACACAGGCCCTTGGGAGACCTTTGGATC 1010

## RESULT 13

US-09-272-796-12  
Sequence 12, Application US/09272796  
Patent No. 6207148  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Corley, Neil C.  
APPLICANT: Guegler, Karl G.  
APPLICANT: Lal, Preeti  
APPLICANT: Goli, Surya K.  
APPLICANT: Shah, Purvi  
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/272,796  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/878,989  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0321 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:





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QY 94 ThrGlyGlyLeuPheGluAspIleValAlaAraGluTyrTyrSerGluAlaAspAla 113
DB 480 ACGGTGGCGAGCTTTTGACCGCATCATGGAGCGCGCTCTCTACACAGAGAAGATGCC 539
QY 114 SerHisCysIleGlnIleLeuGluAlaValLeuHisCysHisGlnMetGlyValVal 133
DB 540 AGCATCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 599
QY 134 HisArgAspLeuLysProGluAsnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 153
DB 600 CACCGGAGCTCAACCGCGAAACCTCTCTGTATGCCAGCGCTTGGAGGACTCGAAGATC 659
QY 154 LysLeuAlaAspPheGlyLeuAlaIleGluValGlnGlyAspGlnGlnAlaTrpPheGly 173
DB 660 ATGCTCTCTGACTTTGGACTCTCC---AAATCCAGGCTGGGAACATG-----CTAGGC 710
QY 174 PheAla---GlyThrProGlyLeuSerProGluValLeuAlaGlyGlyGluAlaTrpGly 192
DB 711 ACCGCTGTGGGAGCCCTGGATATGTGGCCCGCAGAGCTTGTGGAGCAGAACCTACGGG 770
QY 193 LysProValAspIleTrpAlaCysGlyValIleLeuTyrIleLeuValGlyTyrPro 212
DB 771 AAGGCTGTAGATGTGTGGCCCGTGGCGCTCATCTCTACATCCCTGCTGTGGGTACCCC 830
QY 213 ProPheTrpAspGluAspGlnHisLysLeuTyrGlnGlnIleLysAlaGlyAlaTrpAsp 232
DB 831 CCCTTACGACGAGAGCGACCCCTGAGCTCTTCAGCCAGATCCTGAGGCGCAGCTATGAG 890
QY 233 PheProSerProGluTrpAspThrValThrProGluAlaLysAsnLeuLeuAsnGlnMet 252
DB 891 TTTGACTNCTCTTTCTGGGATGACATCTCAGAAATCAGGCAAGAGCTTTATTCGGCAGCT 950
QY 253 LeuThrIleAsnProAlaLysArgIleThrAlaHisGluAlaLeuLysHisProTrpVal 272
DB 951 CTGGAGCGAGACCTTCAGAGAGTTCACCTGCCAACAGGCTTGGGAGCTTTGGATC 1010

RESULT 15
US-08-464-164-1
; Sequence 1, Application US/08464164
; Patent No. 5614195
; GENERAL INFORMATION:
; APPLICANT: Tomley, Fiona M.
; APPLICANT: Dunn, Paul P. J.
; APPLICANT: Bumstead, Janene M.
; APPLICANT: Vermeulen, Arno N.
; TITLE OF INVENTION: Coccidiosis poultry vaccine
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 5614195el Patent Department
; STREET: 1300 Piacard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,164
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gotmley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 258-5200
; INFORMATION FOR SEQ ID NO: 1:
; LENGTH: 1400 base pairs
; TYPE: nucleic acid

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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
ORGANISM: Eimeria maxima
STRAIN: Houghton
DEVELOPMENTAL STAGE: sporozoite
IMMEDIATE SOURCE:
LIBRARY: sporozoite cDNA cloned in Lambda ZAPII
CLONE: Em70-1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1368
US-08-464-164-1

Alignment Scores:
Pred. No.: 6,11e-48 Length: 1400
Score: 529.00 Matches: 139
Percent Similarity: 47.65% Conservative: 94
Best Local Similarity: 28.43% Mismatches: 156
Query Match: 19.48% Indels: 100
DB: 1 Gaps: 15

US-09-820-790b-2 (1-516) x US-08-464-164-1 (1-1400)
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QY 51 SerAlaArg---AspHisGlnLysLeuGluArgIleCysArgLeuLys 69
DB 94 AACACAGACAGATTAAGATATATTAATAAGAGCTTGAATTAATAAGAAATTAAT 153
QY 70 HisSerAsnIleValArgLeuHisAspSerIleSerGluGluGlyPheHisLysVal 89
DB 154 CATCTTAATATCATGAATATATATGAATCTTTGAGGATAAGAGTACTTTTATCTTGT 213
QY 90 PheAspLeuValThrGlyGlyGluLeuPheGluAspIleValAlaArgLysTyrSer 109
DB 214 ACAGAGATATATACAGGAGGAGATATATGATGAATATATTAATCGAAAGATTCAGC 273
QY 110 GluAlaAspAlaSerHisCysIleGlnIleLeuGluAlaValLeuHisCysHisGln 129
DB 274 GAGCGGATGACGCTCGTATAGTACGCTCTATCGGGTATAAATATATATGATCATCGT 333
QY 130 MetGlyValValHisArgAspLeuLysProGluAsnLeuLeuAlaSerLysCysLys 149
DB 334 ATAAATAGTTCATAGAGATTAAGCCAGAGATTTATTTAGAGATATAAAAAA 393
QY 150 GlyAlaAlaValLysLeuAlaAspPheGlyLeuAlaIleGluValGlnGlyAspGln 169
DB 394 GATGCAATATACGAATTATGATTTGGTATCTACACATTTTGAG---CCCCAAAA 450
QY 170 AlaTrpPheGlyPheAlaGlyThrProGlyTyrLeuSerProGluValLeuArgLysGlu 199
DB 451 AAAATGAAGAGATAAAATCGGGACCGCTACTACATTCCTCCCTGAGTGTGCAC---GGA 507
QY 190 AlaTrpGlyLysProValAspIleTrpAlaCysGlyValIleLeuTyrIleLeuVal 209
DB 508 ACATACGATGAGAAATCGGAGCTGTGGTCTAGCGGTGTATCTCTATATCTCTCTCT 567
QY 210 GlyTyrProPheTrpAspGluAspGlnHisLysLysTyrGlnGlnIleLysAlaGly 229
DB 568 GGTGTCTCTCCATTAAACGAGCAATGAATTTGAAATTTCTAAAGAAAGTGCAGAAAGGA 627
QY 230 AlaTyrAspPheProSerProGluTrpAspThrValThrProGluAlaLysLeuIle 249
DB 628 AAATTCACCTTTCGATTTACACAGTGGCGTAAAGTTAGCGAGCCAGCAAGATTTAAT 687
QY 250 AsnGlnMetLeuThrIleAsnProAlaLysArgIleThrAlaHisGluAlaLeuLysHis 269

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GenCore version 5.1.6  
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Ygapop 10.0, Ygapext 0.5  
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Searched: 1731049 seqs, 1297405648 residues

Total number of hits satisfying chosen parameters: 3462098

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2\_6/ptodata/2/pubpna/US05\_NEW\_PUB.seq.\*
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- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
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- 16: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 17: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	2715	100.0	2218	12 US-09-820-790-1 Sequence 1, Appli

2	2225.5	82.0	2061	13	US-10-096-960-1	Sequence 1, Appli
3	2186.5	80.5	3705	13	US-10-044-090-227	Sequence 227, App
4	2177	80.2	5637	10	US-09-917-800A-1537	Sequence 1537, Ap
5	2070	76.2	1500	12	US-10-354-358-87	Sequence 87, Appl
6	2070	76.2	1500	12	US-10-393-892-1	Sequence 1, Appli
7	2070	76.2	1500	12	US-10-394-382-1	Sequence 1, Appli
8	1568	57.8	1551	9	US-09-925-299-210	Sequence 210, App
9	1568	57.8	1551	11	US-09-925-299-210	Sequence 210, App
10	718	26.4	474	11	US-09-918-995-316	Sequence 316, App
11	628.5	23.1	1772	14	US-10-024-036B-1	Sequence 1, Appli
12	619.5	22.8	1694	12	US-10-355-975-3	Sequence 3, Appli
13	618.5	22.8	435	10	US-09-764-868-184	Sequence 184, App
14	618	22.8	1578	9	US-09-835-788A-6	Sequence 6, Appli
15	618	22.8	1578	12	US-10-175-042-6	Sequence 6, Appli
16	616.5	22.7	1733	14	US-10-037-270-526	Sequence 526, App
17	616	22.7	1740	12	US-10-320-351-13	Sequence 13, Appl
18	616	22.7	1740	12	US-10-320-351-14	Sequence 14, Appl
19	613.5	22.6	1074	14	US-10-024-036B-3	Sequence 3, Appli
20	608	22.4	753	9	US-09-910-943-333	Sequence 333, App
21	590.5	21.7	3552	10	US-09-934-406-1	Sequence 1, Appli
22	590.5	21.7	3552	12	US-10-170-789-20	Sequence 20, Appl
23	586.5	21.6	2298	10	US-09-975-326-3	Sequence 3, Appli
24	586.5	21.6	2301	10	US-10-217-357-3	Sequence 3, Appli
25	586.5	21.6	2301	10	US-09-975-326-1	Sequence 1, Appli
26	586.5	21.6	2301	10	US-09-934-406-3	Sequence 3, Appli
27	586.5	21.6	2301	12	US-10-170-789-22	Sequence 22, Appl
28	586.5	21.6	2301	14	US-10-217-357-1	Sequence 1, Appli
29	584.5	21.5	1383	11	US-09-935-464-2	Sequence 2, Appli
30	584.5	21.5	1383	14	US-10-125-835-2	Sequence 2, Appli
31	584.5	21.5	1480	12	US-10-204-041-9	Sequence 9, Appli
32	584.5	21.5	1738	11	US-09-935-464-4	Sequence 4, Appli
33	584.5	21.5	1738	14	US-10-125-835-4	Sequence 4, Appli
34	574.5	21.2	1635	10	US-09-938-842A-2344	Sequence 2344, Ap
35	572.5	21.1	1458	12	US-09-735-138-5	Sequence 5, Appli
36	571	21.0	2165	14	US-10-037-270-809	Sequence 809, App
37	566.5	20.9	1486	10	US-09-938-842A-704	Sequence 704, App
38	566.5	20.9	1747	12	US-10-289-172-2	Sequence 2, Appli
39	566.5	20.9	1747	12	US-09-848-806-2	Sequence 2, Appli
40	565.5	20.8	28438	12	US-09-820-790-3	Sequence 3, Appli
41	563	20.7	1602	10	US-09-938-842A-2304	Sequence 2304, Ap
42	561.5	20.7	1657	12	US-10-289-172-4	Sequence 4, Appli
43	561.5	20.7	1657	12	US-09-848-806-4	Sequence 4, Appli
44	549	20.2	3124	13	US-10-153-921-1	Sequence 1, Appli
45	548	20.2	1372	10	US-09-847-181-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-820-790-1  
; Sequence 1, Application US/09820790  
; Publication No. US20030140354A1  
; GENERAL INFORMATION:

; APPLICANT: SHAO, Wei et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: THEREOF  
; FILE REFERENCE: CLO01204  
; CURRENT APPLICATION NUMBER: US/09/820,790  
; CURRENT FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2218  
; TYPE: DNA  
; ORGANISM: Human  
US-09-820-790-1

Alignment Scores:  
Pred. No.: 1.34e-301 Length: 2218  
Score: 2715.00 Matches: 516  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Oy 1 MetAlaThrValThrcysThrArgPheThrAspGluTyrGlnLeuTyrGluAspIle 20  
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Db 113 ATGGCCACCGGCCACTGCACCGGTTCACGACGACTACCAGCTCTTCGAGGAGTT 172  
  
Oy 21 GlyLvsGlyAlaPheSerValValArqArqCysVallvsLeuCysThrGlvHisGluTrv 40

Db 173 GCAAGGCTGTTCTCTGTCGTCAGGCTGTGAGAAACCTCCACGAGAGTAC 232  
QY |||||  
Db 41 AlaAlaLysLlelleAsnThrLysLysLeuSerAlaArgAspHisGlnLysLeuGluArg 60  
Db 233 GCAGCAAAATCATCAATACCAAGAAATGTCTGCCGGATCACCAGAACTAGAACGT 292  
QY 61 GluAlaArgLleCysArgLeuLeuLysHisSerAsnLleValArgLeuHisAspSerIle 80  
Db 293 GAGGCTCGGATATGTCGACTTCGAAACATCCAAACATCTGTCGCTCCATGACAGTATT 352  
QY 81 SerGluGluGlyPheHisTyrLeuValPheAspLeuValThrGlyGlyLeuLeuPheGlu 100  
Db 353 TCTGAAGAAGGGTTTCACTACCTCGTGTGTTGACCTGTGTACCGCGGGAGCTGTTTCAA 412  
QY 101 AspLleValAlaArgGluTyrTyrSerGluAlaAspAlaSerHisCysLleGlnLle 120  
Db 413 GACATTGGCCAGAGAGTACTACAGTGAAGCAGATGCCAGCCACTGTATACATGATT 472  
QY 121 LeuGluAlaValLeuHisCysHisGlnMetGlyValValHisArgAspLeuLysProGlu 140  
Db 473 CTGGAGAGTGTACCATCCACAGCATGACATCTCCACAGGACCTGAGGCTGAG 532  
QY 141 AsnLeuLeuLeuAlaSerLysCysLysGlyAlaAlaValLysLeuAlaAspPheGlyLeu 160  
Db 533 AACCTGCTGCTGGGAGTAAATGCAAGGGTGCCTGCTCAAGCTGGCTGATTTGGCCTA 592  
QY 161 AlaLleGluValGlnGlyAspGlnAlaTyrPheGlyPheAlaGlyThrProGlyTyr 180  
Db 593 GCATCGAAGTAGTAGGAGAGACAGCAGGCTTGTGTTGTTGTCGCAACCCAGGTTAC 652  
QY 181 LeuSerProGluValLeuArgLysGluAlaTyrGlyLysProValAspLleThrAlaCys 200  
Db 653 TTGTCCTGAGGCTTGTGGAAGAATCCCTATGGAACCTGTGGATATCTGGGCTGC 712  
QY 201 GlyValLleLeuTyrLleLeuLeuValGlyTyrProPheThrAspGluAspGlnHis 220  
Db 713 GGGGTATCTGTATATCTCTGCTGGTGGCTATCTCTGATGAGGATCAGCAC 772  
QY 221 LysLeuTyrGlnGlnLleLysAlaGlyAlaTyrAspPheProSerProGluThrAspThr 240  
Db 773 AAGCTGTATCAGAGATCAAGGCTGGAGCTATGATTTCCTCATCACCAGATGGGACAG 832  
QY 241 ValThrProGluAlaLysAsnLeuLleAsnGlnMetLeuThrLleAsnProAlaLysArg 260  
Db 833 GTAACCTGAGGACCAAGAACTTGATCAACAGAGATCTGACCATAAACCCAGCAAGCGC 892  
QY 261 IleThrAlaHisGluAlaLeuLysHisProThrValCysGlnArgSerThrValAlaSer 280  
Db 893 ATCAGGCTGACACAGGCTCTCAAGCACCCGCTGCTCAACGATCCAGGTGGCATCC 952  
QY 281 MetMetHisArgGlnGluThrValGluCysLeuLysLysPheAsnAlaArgArgLysLeu 300  
Db 953 ATGATCATCTGTCAGAGACCTGGAGTGTTCGCAAGTTCAATGCCCGGAGAAACATG 1012  
QY 301 LysGlyAlaLleLeuThrThrMetLeuAlaThrArgAsnPheSerValGlyArgGlnThr 320  
Db 1013 AAGGGTGCCATCTCAAGACCATGCTTGTCTCCAGAACTTCTCAGTTGCGAGCCAGAGC 1072  
QY 321 ThrAlaProAlaThrMetSerThrAlaAlaSerGlyThrMetGlyLeuValGluGln 340  
Db 1073 TCCGCCCGCCGCTGCGCTGCGGAGCGCGCGGCTGGCC-----GGGCAAGCT 1123  
QY 341 AlaLysSerLeuLeuAsnLysLysAlaAsp---GlyValLysProGlnThrAsnSerThr 359  
Db 1124 GCCAAAGCTATTGACACAGAGTGGATGGCGGTGTCAAGAAAGAGAGTCCAGTCC 1183  
QY 360 LysAsnSerAlaAlaAlaThrSerProLysGlyThrLeuProProAlaAlaLeuGluPro 379  
Db 1184 AGC-----GTGCACCTAATGGAGCCA 1204  
QY 380 GlnThrThrValLleHisAsnProValAspGlyLleLysGluSerSerAspSerAlaAsn 399  
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Db 1205 CAAACCACTGTGTACACACACAGCTACAGATGGGATCAAGGGCTCCACAGAGAGCTGCAAC 1264  
QY 400 ThrThrLleGluAspGluAspAlaLysAla  
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Db 1265 ACCACACAGAGATGAGGAGCTCAAAAGCTGCCCGCTCCGCACCTGGGAATGGCAGCTCG 1324  
QY 409 -----  
Db 1325 GTGCTGAAGACGAGAGCTCCCGGGACAGACAGCCCCCTCTGCAGGCATGCAGCCCGAG 1384  
QY 410 -----ArgLysGlnGluLleLleLysThrThrGluGlnLeu 421  
Db 1385 CTTTCTCTCTGCTCCTCAGCCATGCGAAACAGGAGATCATTAAGATTACAGAACAGCTG 1444  
QY 422 IleGluAlaValAsnAsnGlyAspPheGluAlaTyrAla  
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Db 1445 ATTGAAGCCATCAACAATGGGACTTTGAGGCTTACAGAGATTGTGTATCAGGCTC 1504  
QY 435 -----Phe 435  
Db 1505 ACTTCTTTGAGCCTGAGGCCCTTGTAACTCTGTGGAGGGATGGATTTCATTAAGTTT 1564  
QY 436 TyrPheGluAsnLeuLeuAlaLysAsnSerLysProLleHisThrThrLleLeuAsnPro 455  
Db 1565 TACTTTGAGAATCTCTGTCTCAAGAACAGCAAGCCTATCCATACCACTCTCTAAACCCA 1624  
QY 456 HisValHisValIleGlyGluAspAlaAlaCysIleAlaTyrIleArgLeuThrGlnTyr 475  
Db 1625 CAGCTCCACAGTGTGGGAGGACGCGCTGCATCGCTCATCTCCCTCACCAGTAC 1684  
QY 476 IleAspGlyGlnGlyArgProArgThrSerGlnSerGluGluThrArgValTrpHisArg 495  
Db 1685 ATCGAGGCGAGGCTGCGCTCGACCCAGTCCAGAAAGAGACCCGGGTCTGGCACCGT 1744  
QY 496 ArgAspGlyLysTrpGlnAsnValHisPheHisCysSerGlyAlaProValAlaProLeu 515  
Db 1745 CGGGATGGCAATGGCTCAATGTCCACTACTCTCAGGGGGCCCTGCCGACCGCTG 1804  
QY 516 Gln 516  
Db 1805 CAG 1807  
RESULT 3  
US-10-044-090-227  
; Sequence 227, Application US/10044090  
; Publication No. US20020137081A1  
; GENERAL INFORMATION:  
; APPLICANT: Olga Bandman  
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION  
; FILE REFERENCE: PA-0028 US  
; CURRENT APPLICATION NUMBER: US/10/044, 090  
; CURRENT FILING DATE: 2002-01-09  
; NUMBER OF SEQ ID NOS: 850  
; SOFTWARE: PERL Program  
; SEQ ID NO 227  
; LENGTH: 3705  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. US20020137081A1 327567.50  
US-10-044-090-227  
Alignment Scores:  
Pred. No.: 1,8e-240 Length: 3705  
Score: 2186.50 Matches: 421  
Percent Similarity: 81.18% Conservatives: 19  
Best Local Similarity: 77.68% Mismatches: 29  
Query Match: 80.53% Indels: 73  
DB: 13 Gaps: 3  
US-09-820-790B-2 (1-516) x US-10-044-090-227 (1-3705)

QY 1 MetAlaThrThrValThrCysThrArgPheThrAspGluThrGlnLeuThrGluAspIle 20  
 Db 83 HFGGCAACCCCHCCCTCCGCTTCCAGAGACTACCACTCTTCGAGGAGCTT 142  
 QY 21 GlyLysGlyAlaPheSerValValArgCysValLysLeuCysThrGlyHisGluThr 40  
 Db 143 GCGAGGGTCTCTCTCTGTCGCGAGGTGTGAAGAAACCTCCACGAGGAGTAC 202  
 QY 41 AlaAlaLysIleIleAsnThrLysLysLeuSerAlaArgAspHisGlnLysLeuGluArg 60  
 Db 203 CGACGAAATATCAATACCAAGAAATTTCTGCCGGGATCCACGAAACTAGAACGT 262  
 QY 61 GluAlaArgIleCysArgLeuLeuLysHisSerAsnIleValArgLeuHisAspSerIle 80  
 Db 263 GAGGCTCGATATGCTGTAACATCCAAACATCGTCGCCCTCCATGACATATT 322  
 QY 81 SerGluGluGlyPheHisThrLeuValPheAspLeuValThrGlyGlyGluLeuPheGlu 100  
 Db 323 TCTGAAGAAGGGTTTCACTACCTGCTGTTGACCTTGTACCGGGGGAGCTGTTTGA 382  
 QY 101 AspIleValAlaArgGluThrTy-SerGluAlaAspAlaSerHisCysIleGlnIle 120  
 Db 383 GACATTGTGGCCAGAGACTACTACAGTGAAGGAGTCCAGCCACTGTATACATCAGATT 442  
 QY 121 LeuGluAlaValLeuHisCysHisGlnMetGlyValValHisArgAspLeuLysProGlu 140  
 Db 443 CTGGAGAGTGTAAACACATCCACGACATGACATGCTCCACAGGAGCTGAAGCCTGAG 502  
 QY 141 AsnLeuLeuLeuAlaSerLysCysLysGlyAlaAlaValLysLeuAlaAspPheGlyLeu 160  
 Db 503 AACCTGCTGTCGAGTAAATGCAAGGGTGCCTGCTCAAGCTGCTGATTTTGGCCATA 562  
 QY 161 AlaIleGluValGlnGlyAspGlnAlaThrPheGlyPheAlaClyThrProGlyThr 180  
 Db 563 GCAATCGAAGTACAGGAGAGCAGCAGGCTGCTGTTGTTGCTGTCGACCCAGGTTAC 622  
 QY 181 LeuSerProGluValLeuArgLysGluAlaThrGlyLysProValAspIleThrAlaCys 200  
 Db 623 ATGTCCTCTGAGTCTGTGAGAAAGATCCCTATGGAACCTGTGTGATATCTGGGCTGC 682  
 QY 201 GlyValIleLeuThrValGlyThrProProPheThrAspGluAspGlnHis 220  
 Db 683 GGGGTATCTGTATATCTCTCTGGGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 742  
 QY 221 LysLeuThrGlnGlnIleLysAlaGlyAlaThrAspPheProSerProGluThrAspThr 240  
 Db 743 AAGCTGTATCAGCAGATCAAGCTGAGGCTGATGATTTCCCATCCAGAAATGGAGACG 802  
 QY 241 ValThrProGluAlaLysAsnLeuIleAsnGlnMetLeuThrIleAsnProAlaLysArg 260  
 Db 803 GTAACTCTGAGCCAGACCTTGATCAACAGATGCTGACCATTAACCCAGCAAGCGC 862  
 QY 261 IleThrAlaHisGluAlaLeuLysHisProThrValCysGlnArgSerThrValAlaSer 280  
 Db 863 ATCAGGCTGACGAGGCTCTCAAGCACCCCTGGTGTGTCAACGATCCACGCTGGCATCC 922  
 QY 281 MetMetHisArgGlnGluThrValGluCysLeuLysLysPheAsnAlaArgLysLeu 300  
 Db 923 ATGATGATGCTCAGGAGACTGTGAGGTGTGGCAAGTTCAATGCCCGGAGAAACTG 962  
 QY 301 LysGlyAlaIleLeuThrThrMetLeuAlaThrArgAsnPheSerValGlyArgGlnThr 320  
 Db 983 AAGGTCCTCTCTCAGCAGCTGCTGCTCAGCAAGTCTCTCAGCT----- 1030  
 QY 321 ThrAlaProAlaThrMetSerThrAlaAlaSerGlyThrThrMetGlyLeuValGluGln 340  
 Db 1030 ----- 1030  
 QY 341 AlaLysSerLeuLeuAsnLysLysAlaAspGlyValLysProGluThrAsnSerThrLys 360  
 Db 1031 GCGAAAGGCTATTGAAAGAGTGGATGCG----- 1063  
 QY 361 AsnSerAlaAlaAlaThrSerProLysGlyThrLeuProProAlaAlaLeuGluProGln 380

Db 1064 -----GGTGTCAAGAGACCAAA 1081  
 QY 381 ThrThrValIleHisAsnProValAspGlyLysGluSerSerSerSeraIleAsnThr 400  
 Db 1082 ACCACTGTGTACACACGCTACAGATGGATCAAGGGCTCCACAGAGAGCTCAACAC 1141  
 QY 401 ThrIleGluAspGluAspAlaLysAlaArgLysGlnGluIleLysThrThrGluGln 420  
 Db 1142 ACCACGAGAAGTGAAGGACCTCAAGTCCGAAACAGAGAGATCATTAAGATTACAGAACAG 1201  
 QY 421 LeuIleGluAlaValAsnAsnGlyAspPheGluAlaValAla----- 434  
 Db 1202 CTGATTGAAGCCATCAACATGGGGACTTTGAGGCCCTACACGAGATTGTGTATCCAGGC 1261  
 QY 434 ----- 434  
 Db 1262 CTCACCTCCCTTTGAGCCCTGAGGCCCTTGGTAACTCGTGGAGGGGATGGATTTCCATAAG 1321  
 QY 435 PheTy-PheGluAsnLeuLeuAlaLysAsnSerLysProIleHisThrThrIleLeuAsn 454  
 Db 1322 TTATTCTTTGAGAATCTCTCTCCACAGACAGCAAGCCTATCCATACCACATCCTTAAC 1381  
 QY 455 ProHisValHisValIleGlyGluAspAlaAlaCysIleAlaTyIleArgLeuThrGln 474  
 Db 1382 CCACAGCTCCAGCTGATTGGGGAGAGCGAGCGTGCATCGCTACATCCGCTCAAGCCAG 1441  
 QY 475 TyrIleAspGlyGlnGlyArgProArgThrSerGlnSerGluThrArgValThrPheHis 494  
 Db 1442 TACATCGAGCGAGGTCGGCTCCGCCAGCCAGTCCAGAGAGACCCGGGTCTGGCAC 1501  
 QY 495 ArgArgAspGlyLysThrGlnAsnValHisPheHisCysSerGlyAlaProValAlaPro 514  
 Db 1502 CGTGGGAGTGAAGTGTCTCAATCTCCACTATCACTGTCAGGGGCGCTCGCCGACCG 1561  
 QY 515 LeuGln 516  
 Db 1562 CTGCAG 1567  
 RESULT 4  
 US-09-917-800A-1537  
 : Sequence 1537, Application US/09917800A  
 : Patent No. US20020119462A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Mendrick, Donna  
 : APPLICANT: Porter, Mark  
 : APPLICANT: Johnson, Kory  
 : APPLICANT: Castile, Arthur  
 : APPLICANT: Elashoff, Michael  
 : APPLICANT: Gene Logic, Inc.  
 : TITLE OF INVENTION: Molecular Toxicology Modeling  
 : FILE REFERENCE: 44921-5038-US  
 : CURRENT APPLICATION NUMBER: US/09/917,800A  
 : CURRENT FILING DATE: 2001-07-31  
 : PRIOR APPLICATION NUMBER: US 60/222,040  
 : PRIOR FILING DATE: 2000-07-31  
 : PRIOR APPLICATION NUMBER: US 60/222,880  
 : PRIOR FILING DATE: 2000-11-02  
 : PRIOR APPLICATION NUMBER: US 60/290,029  
 : PRIOR FILING DATE: 2001-05-11  
 : PRIOR APPLICATION NUMBER: US 60/290,645  
 : PRIOR FILING DATE: 2001-05-15  
 : PRIOR APPLICATION NUMBER: US 60/292,336  
 : PRIOR FILING DATE: 2001-03-22  
 : PRIOR APPLICATION NUMBER: US 60/295,798  
 : PRIOR FILING DATE: 2001-06-06  
 : PRIOR APPLICATION NUMBER: US 60/297,457  
 : PRIOR FILING DATE: 2001-06-13  
 : PRIOR APPLICATION NUMBER: US 60/298,884  
 : PRIOR FILING DATE: 2001-06-19  
 : PRIOR APPLICATION NUMBER: US 60/303,459  
 : PRIOR FILING DATE: 2001-07-09  
 : NUMBER OF SEQ ID NOS: 1740

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1537
; LENGTH: 5637
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_012519
US-09-917-800A-1537

Alignment Scores:
Pred. No.: 4,31e-239 Length: 5637
Score: 2177.00 Matches: 420
Percent Similarity: 83.21% Conservative: 31
Best Local Similarity: 77.49% Mismatches: 35
Query Match: 80.18% Indels: 6
DB: 10 Gaps: 6

US-09-820-790B-2 (1-516) x US-09-917-800A-1537 (1-5637)
QY 1 MetAlaThrValThrCysThrArgPheThrAspGluTyrGlnLeuTyrGluAspIle 20
DB 223 ATGGGTTGACACACACCTCCACCGCGTTTCACCGACGAGTATCAGCTCTTCGAGGAGTC 282
QY 21 GlyLysGlyAlaPheSerValValArgCysValLysLeuCysThrGlyHisGlnTyr 40
DB 283 GGAAGGGGGCATCTTCAGTGGTGAGACATCATGAATAATCCCTACTGGACAAGATAT 342
QY 41 AlaAlaLysIleLeuAsnThrLysLysLeuSerAlaArgAspHisGlnLysLeuGluArg 60
DB 343 GTGGCAAAATATCAACCAACCAAAAGCTTCTGTAGGGATCATCAGAACTGGAAAGG 402
QY 61 GluAlaArgIleCysArgLeuLeuLysHisSerAsnIleValArgLeuHisAspSerIle 80
DB 403 GAAGTAGAATCTGCCGCTCTCTGAAGCACCCCATATATTGTGAGACTTCATGACAGCAT 462
QY 81 SerGluGluGlyPheHisTyrLeuValPheAspLeuValThrGlyGlyGluLeuPheGlu 100
DB 463 TCGAAGAGGGCTCCATCTACTTGGTGTGTGACTAGTACTGGTGGCAACTCTTTGAA 522
QY 101 AspIleValAlaArgGluTyrTyrSerGluAlaAspAlaSerHisCysIleGlnIle 120
DB 523 GACATAGTGGCAGAGAAATATACAGTGGGCTGATGCGTCACTGATGATGATATACAGAGAT 582
QY 121 LeuGluAlaValLeuHisCysHisGlnMetGlyValValHisArgAspLeuLysProGlu 140
DB 583 CTAGAGAGGTAAATCATTTCTACCTAAATGCGATAGTTCACAGGGACCTGAAGCCTGAG 642
QY 141 AsnLeuLeuLeuAlaSerLysCysGlyAlaAlaValLysLeuAlaAspPheGlyLeu 160
DB 643 AATTTGCTTTTAGCTAGCAATCCAAAGGAGCAGCTGTGAACCTGGCAGACTTCGGCTTA 702
QY 161 AlaIleGluValGlnGlyAspGlnAlaTyrPheGlyPheAlaGlyThrProGlyTyr 180
DB 703 GCCATAGAGTGTAAAGCGACAGCAGCGGTGTTGTTTGTGTCGACACCTGGGAT 762
QY 181 LeuSerProGluValLeuArgLysGluAlaTyrGlyLysProValAspIleThrPalAcys 200
DB 763 CTTTCGCCAAGAGTCTACGTAAGATCCTTATGAAACCCAGTGGACATGTGGCATGT 822
QY 201 GlyValIleLeuTyrIleLeuLeuValGlyTyrProPheThrPaspGluAspGlnHis 220
DB 823 GCGGTATCATCTTCTGCTGGTGGATACCCACCCCTTCTGGGATGAAGATCAGCAT 882
QY 221 LysLeuTyrGlnIleLysAlaGlyAlaTyrAspPheProSerProGluThrPaspThr 240
DB 883 AGACTGTATCAGCAGATCAAGGCTGGGCTACGATTTTCCATCCACAGATGGGACACA 942
QY 241 ValThrProGluAlaLysAsnLeuIleAsnGlnMetLeuThrIleAsnProAlaLysArg 260
DB 943 GTGACACCTGAAGCCAAAGACCTCATCAACAAATGCTGACATCAACCTGCCAACGCC 1002
QY 261 IleThrAlaHisGluAlaLeuLysHisProThrValCysGlnArgSerThrValAlaSer 280

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DB 1003 ATCACAGCCTCTGAGGCCCTGAAACACACCCATGGATCTGTCAACGTTCTACTGTTCCTCC 1062
QY 281 MetMetHisArgGlnGluThrValGluCysLeuLysLysPheAsnAlaArgGlySer 300
DB 1063 ATGATGCACAGGACGAGACTGTAGACTGCTTGAAGAAATTTAATGCTCGAGGAATG 1122
QY 301 LysGlyAlaIleLeuThrThrMetLeuAlaThrArgAsnPheSerValGlyArgGlnThr 320
DB 1123 AAGGGTGCCATCTTGACCACTATGTGCTACGAGAATTTTTCAGCA----- 1170
QY 321 ThrAlaProAlaThrMetSerThrAlaAlaSerGlyThrThrMetGlyLeuValGluGln 340
DB 1170 ----- 1170
QY 341 AlaLysSerLeuLeuAsnLysLysAlaAspGlyValLysProGlnThrAsnSerThrLys 360
DB 1171 GCCAAGAGTTTGTG---AAGAAACCGGATGGGTAAAG-----ATAAACCAACAAAGCC 1221
QY 361 AsnSerAlaAlaAlaThrSerProLysGlyThrLeuProAlaAlaLeuGluProGln 380
DB 1222 AAC-----GTGGTAACCGAGCCCAAGAAATATCTACCCCGCGCTGGAGCCCA 1275
QY 381 ThrThrValIleHisAsnProValAspGlyIleLysGluSerSerAspSerAlaAsnThr 400
DB 1276 ACTACTGTAAATCCACAAGCCT---GATGAAACAAAGAGTCAACTGAGAGCTCAATATACC 1332
QY 401 ThrIleGluAspGluAspAlaLysAlaArgLysGlnIleIleLysThrThrGluGln 420
DB 1333 ACCATTGAGGATGAAGACGTGAAGCAGCAAGCAAGATCATCAAGTCACTGAGCAG 1392
QY 421 LeuIleGluAlaValAsnAsnGlyAspPheGluAlaTyrAla----- 434
DB 1393 CTGATTGAAGTATCAACATGGGACITCGAGGCTTACACGAAATCTGTGATCCAGGC 1452
QY 434 ----- 434
DB 1453 CTCACCTGCTTTGAACCCGAGCACTTGGCAACTTAGTGAAGGGATGGACTTTCACAGA 1512
QY 435 PheTyrPheGluAsnLeuLeuAlaLysAsnSerLysProIleHisThrThrIleLeuAsn 454
DB 1513 TTCTACTTTGAAATGTTTGGCCAAATCAATTAACCAATCCACACTATCATCTGTGAC 1572
QY 455 ProHisValHisValIleGlyGluAspAlaAlaCysIleAlaTyrIleArgLeuThrGln 474
DB 1573 COTCAGCTACACCTGTGTAGGGATGATGACGCTGCATAGCATACATTCGGCTCACACAG 1632
QY 475 TyrIleAspGlyGlnGlyArgProArgThrSerGlnSerGluGlnThrArgValThrHis 494
DB 1633 TCATGGATGAAATGGAATGCCAAGACCAATGCAAGAGACTCGAGTGTGGCNC 1692
QY 495 ArgAlaGspGlyLysTyrGlnAsnValHisPheHisCysSerGlyAlaProValAlaPro 514
DB 1693 CGCGGTGATGGAGTGGCAGATATTCATCTTCATGTCGGGGTCCCCACACAGTCCCC 1752
QY 515 LeuGln 516
DB 1753 ATCAAG 1758

RESULT 5
US-10-354-358-87
; Sequence 87, Application US/10354358
; Publication No. US20030157082A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Hunter, John Joseph
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Lesoon, Andrea
; APPLICANT: Lightcap, Eric S.
; APPLICANT: Williamson, Mark
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,

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; TITLE OF INVENTION: 7161, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,  
 ; TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18994, 2085, 32427, 2160,  
 ; TITLE OF INVENTION: 952, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,  
 ; TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,  
 ; TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,  
 ; TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES  
 ; FILE REFERENCE: MP102-020P1RNMNM  
 ; CURRENT APPLICATION NUMBER: US/10/354,358  
 ; CURRENT FILING DATE: 2003-01-30  
 ; PRIOR APPLICATION NUMBER: US 60/353,600  
 ; PRIOR FILING DATE: 2002-01-31  
 ; PRIOR APPLICATION NUMBER: US 60/364,517  
 ; PRIOR FILING DATE: 2002-03-15  
 ; PRIOR APPLICATION NUMBER: US 60/371,075  
 ; PRIOR FILING DATE: 2002-04-09  
 ; PRIOR APPLICATION NUMBER: US 60/371,507  
 ; PRIOR FILING DATE: 2002-04-10  
 ; PRIOR APPLICATION NUMBER: US 60/372,984  
 ; PRIOR FILING DATE: 2002-04-16  
 ; PRIOR APPLICATION NUMBER: US 60/374,194  
 ; PRIOR FILING DATE: 2002-04-19  
 ; PRIOR APPLICATION NUMBER: US 60/382,995  
 ; PRIOR FILING DATE: 2002-05-24  
 ; PRIOR APPLICATION NUMBER: US 60/385,023  
 ; PRIOR FILING DATE: 2002-05-31  
 ; PRIOR APPLICATION NUMBER: US 60/388,853  
 ; PRIOR FILING DATE: 2002-06-14  
 ; PRIOR APPLICATION NUMBER: US 60/389,395  
 ; PRIOR FILING DATE: 2002-06-17  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 122  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 87  
 ; LENGTH: 1500  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)...(1500)  
 US-10-354-358-87

Alignment Scores:  
 Pred. No.: 1,09e-227 Length: 1500  
 Score: 2070.00 Matches: 396  
 Percent Similarity: 78.78% Conservatives: 31  
 Best Local Similarity: 73.06% Mismatches: 25  
 Query Match: 76.24% Indels: 90  
 DB: 12 Gaps: 3

US-09-820-790B-2 (1-516) x US-10-354-358-87 (1-1500)

QY 1 MetAlaThrThrValThrCysThrArgPheThrAspGluThrGlnLeuThrGluAspIle 20  
 Db 1 ATGGCTTCGACCAACCACCCACCCAGGTTCCAGGACGAGTATCAGCTTTCGAGGAGCTT 60  
 QY 21 GlyValGlyAlaPheSerValValArgCysValLysLeuCysThrGlyHisGluThr 40  
 Db 61 GGAAGGGGGGCTCTCTAGTGGTGGAGAGATGATGAAATTCCTCTGACCAAGGATAT 120  
 QY 41 AlaAlaLysIleIleAsnThrLysLysLeuSerAlaArgAspHisGlnLysLeuGluArg 60  
 Db 121 GCTGCCAATATATCAACCAAAAGCTTTCGCTAGGATATCATCAAACTAGAAAGA 180  
 QY 61 GluAlaArgIleCysArgLeuLysHisSerAsnIleValArgLeuHisAspSerIle 80  
 Db 181 GAAGCTAGAATCTGGCGCTTTTGAAGCAACCTTAATATGTGCGACTTCATGATAGATA 240  
 QY 81 SerCluCluLysPheHisThrLeuValPheAspLeuValThrGlyGluLeuPheGlu 100  
 Db 241 TCAGAAGGGGCTTTCACCTACTTGTGATTTAGTTACTGGAGGTGAACCTTTTGA 300  
 QY 101 AspIleValAlaArgGluThrTyrSerGluAlaAspAlaSerHisCysIleGlnGlnIle 120  
 Db

Db 301 GACATAGTGGCAGAGATACACTACAGTGAAGCTGATGCCAGTCATCTGTATATACAGCAGATT 360  
 QY 121 LeuGluAlaValLeuHisCysHisGlnMetGlyValValHisArgAspLeuLysProGlu 140  
 Db 361 CTAGAAGGTGTAATCATCTGACCTAAATGGCATAGTTCACAGGGACCTGAAGCCTGAG 420  
 QY 141 AsnLeuLeuLeuAlaSerLysCysLysGlyAlaAlaValLysLeuAlaAspPheGlyLeu 160  
 Db 421 AATTTGCTTTTAGCTAGCAATCCAGGGAGCAGCTGTGAAATGGCAGCTTTGGCTTA 480  
 QY 161 AlaIleGluValGlnGlyAspGlnGlnAlaTrpPheGlyPheAlaGlyThrProGlyTyr 180  
 Db 481 GCCATAGAAGTTCAGGGGACCAAGCGCTGTTTGGTTTGGTGGTGGCAGCTGGATAT 540  
 QY 181 LeuSerProGluValLeuArgLysGluAlaTyrGlyLysProValaspIleTrpAlaCys 200  
 Db 541 CTTTCTCCAGAGTTTACGTAAAGATCCTTATGAAAGCCAGTGGATGTGGGCATGT 600  
 QY 201 GlyValIleLeuTyrIleLeuLeuValGlyTyrProPheTrpAspGluaspGlnHis 220  
 Db 601 GGTGTCATCTCTATATCTTACTTGTGGGTATCCACCTTCTGGGATGAAGCAACAC 660  
 QY 221 LysLeuTyrGlnGlnIleLysAlaGlyAlaTyrAspPheProSerProGluTrpAspThr 240  
 Db 661 AGACTCTATCAGCAGATCAAGGCTGGAGCTTATGATTTTCCATCACCAGATGGGACAG 720  
 QY 241 ValThrProGluAlaLysAsnLeuIleAsnGlnMetLeuThrIleAsnProAlaLysArg 260  
 Db 721 GTGACTCCCTGAAGCCAAAGACCTCATCAATAAAATGCTTACTATCAACCTGCCAAAGC 780  
 QY 261 IleThrAlaHisGluAlaLeuLysHisProTrpValCysGlnArgSerThrValAlaSer 280  
 Db 781 ATCAGAGCTCAGAGGACCTGAAGCACCACCATGATCTCAACGCTTCTACTGTGCTCC 840  
 QY 281 MetMetHisArgGlnGluThrValGluCysLeuLysLysPheAsnAlaArgArgLysLeu 300  
 Db 841 ATGATGCACAGACAGGAGACTGTAGACTGCTTGAAGAAATTTAATGCTAGAAGAAACTA 900  
 QY 301 LysGlyAlaIleLeuThrThrMetLeuAlaThrArgAsnPheSerValGlyArgGlnThr 320  
 Db 901 AAGGTGCTCCATCTTGACAACTATGCTGGCTACAAGAAATTTCTCAGCA----- 948  
 QY 321 ThrAlaProAlaThrMetSerThrAlaAlaSerGlyThrThrMetGlyLeuValGluGln 340  
 Db 948 ----- 948  
 QY 341 AlaLysSerLeuLeuAsnLysLysAlaAspGlyValLysProGlnThrAsnSerThrLys 360  
 Db 949 GCCAAGAGTTTCTTGAAGAAACCA----- 972  
 QY 361 AsnSerAlaAlaAlaThrSerProLysGlyThrLeuProProAlaAlaLeuGluProGln 380  
 Db 972 ----- 972  
 QY 381 ThrThrValIleHisAsnProValaspGlyIleLysGluSerSerAspSerAlaAsnThr 400  
 Db 973 -----GATGGAGTAAAGAGTCACTGAGAGTTCATATACA 1008  
 QY 401 ThrIleGluAspGluAspAlaLysAlaArgLysGlnGluIleLysThrThrGluGln 420  
 Db 1009 ACATTTGAGATGAGATGTGAAGCAGCAGCAAGCAGAGATATCAAGAGTCACTGAACA 1068  
 QY 421 LeuIleGluAlaValAsnAsnGlyAspPheGluAlaTyrAla----- 434  
 Db 1069 CTGATCGAAGCTATCAACAATGGGAGCTTTGAAGCTACACAAAATCTGTGACCCAGGC 1128  
 QY 434 ----- 434  
 Db 1129 CTTACTGCTTTTGAACCTGAAAGCTTTGGGTAAATTTAGTGAAGGATGGATTTTCAACGA 1188  
 QY 435 PheTyrPheGluAsnLeuLeuAlaLysAsnSerLysProIleHisThrThrIleLeuAsn 454  
 Db 1189 TTCTACTTGAATATGCTTTGTCCAAAGCAATAAACCATCCACACTATTTATTTCTAAC 1248



QY 455 ProHisValHisValIleGlyGluAspAlaCysIleAlaTyrIleArgLeuThrGln 474  
 DB 1249 CCTCATGTACATCTCTGGTGGGATGATGCCGCTGCATAGCATATATTAGGCTCACACAG 1308  
 QY 475 TyrIleAspGlyGlnGlyArgProArgThrSerGlnSerGluGluThrArgValTrpHis 494  
 DB 1309 TCAATGGATGGCACTGGAAATGCCAAGACATGAGTCAGAGAGACTCGTGTGGGCAC 1368  
 QY 495 ArgArgAspGlyLysTrpGlnAsnValHisPheHisCysSerGlyAlaProValAlaPro 514  
 DB 1369 CGCCGGGATGAAAGTGGCAGAAATGTTTCATTTTCATCGCTCGGGTCAACACAGTACC 1428  
 QY 515 LeuGln 516  
 DB 1429 ATCAAG 1434

RESULT 6  
 US-10-393-892-1  
 ; Sequence 1, Application US/10393892  
 ; Publication No. US20030186302A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WANG, YIXIN  
 ; TITLE OF INVENTION: COLORECTAL CANCER DIAGNOSTICS  
 ; FILE REFERENCE: CDS 267 US NP  
 ; CURRENT APPLICATION NUMBER: US/10/393,892  
 ; CURRENT FILING DATE: 2003-03-21  
 ; PRIOR APPLICATION NUMBER: 60/368,798  
 ; PRIOR FILING DATE: 2002-03-29  
 ; NUMBER OF SEQ IDS: 49  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 1500  
 ; TYPE: DNA  
 ; ORGANISM: human  
 US-10-393-892-1

Alignment Scores:  
 Pred. No.: 1.09e-227 Length: 1500  
 Score: 2070.00 Matches: 396  
 Percent Similarity: 78.78% Conservative: 31  
 Best Local Similarity: 73.06% Mismatches: 25  
 Query Match: 76.24% Indels: 90  
 DB: 12 Gaps: 3

US-09-820-790b-2 (1-516) x US-10-393-892-1 (1-1500)

QY 1 MetAlaThrThrValThrCysThrArgPheThrAspGluThrGlnLeuThrGluAspIle 20  
 DB 1 ATGGCTTCGACCCACCCCTGCACCGAGTTTCAGGACGAGTATCAGCTTTTCAGGAGGCTT 60  
 QY 21 GlyLysGlyAlaPheSerValValArgCysValLysLeuCysThrGlyHisGluThr 40  
 DB 61 GGAAGGGGGCATCTTCAGTGGGAGACATGTATGAAATTCCTACTGGACAAGATAT 120  
 QY 41 AlaAlaLysIleIleAsnThrLysLysLeuSerAlaArgAspHisGlnLysLeuGluArg 60  
 DB 121 GCTGCCAAATATACACCAAAAGCTTTCTGCTAGGGATCATCAGAACTAGAAAAGA 180  
 QY 61 GluAlaArgIleCysArgLeuLeuLysHisSerAsnIleValArgLeuHisAspSerIle 80  
 DB 181 GAAGTAGAATCTGCCGCTCTTTTGAAGCACCCCTAATATGTGGGACTTTCATATAGCAT 240  
 QY 81 SerGluGluGlyPheHisTyrLeuValPheAspLeuValThrGlyGlyGluLeuPheGlu 100  
 DB 241 TCAGAAGAGGGCTTTCATCTACTTGGTGTGTTGATTAGTTACTGGAGGTGAAGTGTGAA 300  
 QY 101 AspileValAlaArgGluThrTyrSerGluAlaAspAlaSerHisCysIleGlnIle 120  
 DB 301 GACATAGTGGCAGAGATATACATCAGTGAAGCTGATGCCATGTTATATACAGAGATT 360  
 QY 121 LeuGluAlaValLeuHisCysHisGlnMetGlyValValHisArgAspLeuLysProGlu 140  
 DB 1249 CCTCATGTACATCTCTGGTGGGATGATGCCGCTGCATAGCATATATTAGGCTCACACAG 1308

DB 361 CTAGAAAGTGTAAATCATTTGTCACCTAAATGGCATAGTTTCACAGGGAGCTGAACCCCTGAG 420  
 QY 141 AsnLeuLeuLeuAlaSerLysCysLysGlyAlaAlaValLysLeuAlaAspPheGlyLeu 160  
 DB 421 AATTTGCTTTTAGTAGCAATCCCAAGGAGCAGCTGTGAAATTTGCAGACTTTTGGCTTA 480  
 QY 161 AlaIleGluValGlnGlyAspGlnAlaThrPheGlyPheAlaGlyThrProGlyTyr 180  
 DB 481 GCCATAGAAATTCAGGGGACCAGCAGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 540  
 QY 181 LeuSerProGluValLeuArgLysGluAlaTyrGlyLysProValAspIleTrpAlaCys 200  
 DB 541 CTTTCTCCAGAGCTTTTACGTHAAGATCCTTATGGAAGCCAGTGGATATGTGGCATGT 600  
 QY 201 GlyValIleLeuTyrIleLeuLeuValGlyTyrProPheTrpAspGluAspGlnHis 220  
 DB 601 GGTGTCTATTTCTATATTTCTACTTGTGGGTATCCACCTTCTGGGTGAAGACCAACAC 660  
 QY 221 LysLeuTyrGlnGlnIleLysAlaGlyValAspPheProSerProGluTrpAspThr 240  
 DB 661 AGACTCTATCAGCAGATCAAGCTGGAGCTTATGATTTTCCATCACCAGATGGACAG 720  
 QY 241 ValThrProGluAlaLysAsnLeuLeuMetLeuThrIleAsnProAlaLysArg 260  
 DB 721 GTGACTCTGAAGCCAAAGACCTCATCAATAAATGCTTACTATCAACCTGCCAAACGC 780  
 QY 261 IleThrAlaHisGluAlaLeuLysHisProTrpValCysGlnArgSerThrValAlaSer 280  
 DB 781 ATCAGGCTCAGAGCAGTGAAGCACCAGTGGATCTGTCACAGTCTTACTTGTGCTTCC 840  
 QY 281 MetMetHisArgGlnGluThrValGluCysLeuLysLysPheAsnAlaArgGlyLeu 300  
 DB 841 ATGATGCACACAGAGGAGACTGTAGACTGCTGAAGAAATTAATGCTAGAGAAACTA 900  
 QY 301 LysGlyAlaIleLeuThrThrMetLeuAlaThrArgAsnPheSerValGlyArgGlnThr 320  
 DB 901 AAGGGTGCCATCTGTGCAACTATGCTGTGCTACAGGAATTTCTCAGCA----- 948  
 QY 321 ThrAlaProAlaThrMetSerThrAlaAlaSerGlyThrThrMetGlyLeuValGluGln 340  
 DB 948 ----- 948  
 QY 341 AlaLysSerLeuLeuAsnLysLysAlaAspGlyValLysProGlnThrAsnSerThrLys 360  
 DB 949 GCCAAGAGTGTGTGAAGAAACCA----- 972  
 QY 361 AsnSerAlaAlaAlaThrSerProLysGlyThrLeuProAlaAlaLeuGluProGln 380  
 DB 972 ----- 972  
 QY 381 ThrThrValIleHisAsnProValAspGlyIleLysGluSerSerAspSerAlaAsnThr 400  
 DB 973 -----GATGGACTAAAGGAGTCAACTGAGAGTCAATATCA 1008  
 QY 401 ThrIleGluAspGluAspAlaLysAlaArgLysGlnIleIleLysThrGluGln 420  
 DB 1009 ACAATTTAGGATGAGATGTGAAGCAGCAAGCAAGAGATTATCAAACTCACTGAACAA 1068  
 QY 421 LeuIleGluAlaValAsnAsnGlyAspPheGluAlaTyrAla----- 434  
 DB 1069 CTGATCGAGTATCAACAATGGGACTTTGAACCTTACACAAATCTGTGACCCAGGC 1128  
 QY 434 ----- 434  
 DB 1129 CTTACTGCTTTGAACCTGAAGCTTTGGGTAAATTTAGTGGAGGGATGGATTTTCAACGA 1188  
 QY 435 PheTyrPheGluAsnLeuLeuAlaLysAsnSerLysProIleHisThrThrIleLeuAsn 454  
 DB 1189 TTTCTACTTTGAAATGCTTTGTCCAAAGCAATTAACCAATCCACACTATTATTCTTAAC 1248  
 QY 455 ProHisValHisIleGlyGluAspAlaAlaCysIleAlaTyrIleArgLeuThrGln 474  
 DB 1249 CCTCATGTACATCTCTGGTGGGATGATGCCGCTGCATAGCATATATTAGGCTCACACAG 1308

QY 475 TyrIleAspGlyGlnGlyArgProArgThrSerGlnSerGluGluThrArgValTrpHis 494  
 Db 1309 TACATGATGGCAGTGAATGCCAAGACAAATGCATCAGAGAGACTCGTGTGGGCAC 1368  
 QY 495 ArgArgAspGlyLysTrpGlnAsnValHisPheHisCysSerGlyAlaProValAlaPro 514  
 Db 1369 GCCGGGATGGAAAGTGGCAGAAATGTTCAATTCATCGCTCGGGGTCAACCAACAGTACCC 1428  
 QY 515 LeuGln 516  
 Db 1429 ATCAAG 1434

## RESULT 7

US-10-394-382-1  
 ; Sequence 1, Application US/10394382  
 ; Publication No. US20030186303A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Yixin  
 ; TITLE OF INVENTION: COLORECTAL CANCER DIAGNOSTICS  
 ; FILE REFERENCE: CDS 266 US NP  
 ; CURRENT APPLICATION NUMBER: US/10/394,382  
 ; CURRENT FILING DATE: 2003-03-21  
 ; PRIOR APPLICATION NUMBER: 60/368,687  
 ; PRIOR FILING DATE: 2002-03-29  
 ; NUMBER OF SEQ ID NOS: 49  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 1500  
 ; TYPE: DNA  
 ; ORGANISM: human  
 US-10-394-382-1

## Alignment Scores:

Pred. No.: 1,09e-227 Length: 1500  
 Score: 2070.00 Matches: 336  
 Percent Similarity: 78.78% Conservative: 31  
 Best Local Similarity: 73.06% Mismatches: 25  
 Query Match: 76.24% Indels: 90  
 DB: 12 Gaps: 3

US-09-820-790B-2 (1-516) x US-10-394-382-1 (1-1500)

QY 1 MetaIaThrValThrCysThrArgPheThrAspGluThrGlnLeuThrGluAspIle 20  
 Db 1 ATGGCTTCGACCAACCCCTGCACCGAGTTCACGGAGAGTATCAGCTTTTCGAGGAGCT 60  
 QY 21 GlyLysGlyAlaPheSerValValArgArgCysValLysLeuCysThrGlyHisGluTyr 40  
 Db 61 GGAAGGGGGCATCTTCAGTGTGAGAGATGATGAAATTCCTACTGGCAAGGATAT 120  
 QY 41 AlaAlaLysIleIleAsnThrLysLysLeuSerAlaArgAspHisGlnLysLeuGluArg 60  
 Db 121 GTGCGCAAAATTAACACACCAAGAGCTTTCTGCTAGGGATCATCGAAACTAGAAAGA 180  
 QY 61 GluAlaArgIleCysArgLeuLeuLysHisSerAsnIleValArgLeuHisAspSerIle 80  
 Db 181 GAAGTAGATCTGCCGTCTTTTGAAGCACCCCTAATATGTGCGACTTCATGATAGCA 240  
 QY 81 SerGluGluGlyPheHisTyrLeuValPheAspLeuValThrGlyGlyGluLeuPheGlu 100  
 Db 241 TCAGAAGAGGGCTTTCATCTACTTGTGTTGATTTAGTTACTGGAGGTGAATCTTTTGA 300  
 QY 101 AspIleValAlaArgGluTyrTyrSerGluAlaAspAspHisCysIleGlnIle 120  
 Db 301 GACATAGTGGCAAGAGAACTACAGTGAAGCTGATGCCCATCTGTTATACAGCAGATT 360  
 QY 121 LeuGluAlaValLeuHisCysHisGlnMetGlyValValHisArgAspLeuProGlu 140  
 Db 361 CTAGAAGGTGTATCATTTGTCACCTAATGGCATAGTTTCACAGGGAGCTGAAGCCGAG 420  
 QY 141 AsnLeuLeuLeuAlaSerLysCysLysGlyAlaValLysLeuAlaAspPheGlyLeu 160

Db 421 AATTTGCTTTTAGCTAGCAAAATCCAAAGGAGCAGCTGTGAAATTTGGCAGACTTTGGCCTTA 480  
 QY 161 AlaIleGluValGlnGlyAspGlnGlnAlaTrpPheGlyPheAlaGlyThrProGlyTyr 180  
 Db 481 GCCATAGAAGTTCGAAGGGGACCAGCAGCGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540  
 QY 181 LeuSerProGluValLeuLeuGlyLysGluAlaTyrGlyLysProValAspIleTrpAlaCys 200  
 Db 541 CTTTCTCCAGAGTTTACGTAAGAATCCCTTATGAAGCCAGTCAGTATATGCGCATGT 600  
 QY 201 GlyValIleLeuTyrIleLeuLeuValGlyTyrProPheTrpAspGluAspGlnHis 220  
 Db 601 GGTGTCAATCTCTATATTTCTACTTGTGGGTATCCACCTTCTGGATGAGACCAACAC 660  
 QY 221 LysLeuTyrGlnGlnIleLysAlaGlyAlaTyrAspPheProSerProGluTrpAspThr 240  
 Db 661 AGACTCTATCAGCAGATCAGGCTGGAGCTTAATGATTTTCCATCACCAGATGGGACAG 720  
 QY 241 ValThrProGluAlaLysAsnLeuIleAsnGlnMetLeuThrIleAsnProAlaLysArg 260  
 Db 721 GTGACTCTCTGAAGCCAAAGACCTCATCAATAAATGCTTACTATCAACCTGCCAAACGC 780  
 QY 261 IleThrAlaHisGluAlaLeuLysHisProTrpValCysGlnArgSerThrValAlaSer 280  
 Db 781 ATCAGAGCTCAGAGGCACCTGAAGCACCACCATGGATCTGCAACGTTCTACTTCTCTCC 840  
 QY 281 MetMetHisArgGlnGluThrValGluCysLeuLysLysPheAsnAlaArgArgLysLeu 300  
 Db 841 ATGATCCACAGACAGGAGACTGTAGACTGCTTGAAGAAATTTAATGCTAGAGAAACTA 900  
 QY 301 LysGlyAlaIleLeuThrThrMetLeuAlaThrArgAsnPheSerValGlyArgGlnThr 320  
 Db 901 AAGGTTGCCATCTTGACAACTATGCTGGCTACAGAAATTTCTCAGCA----- 948  
 QY 321 ThrAlaProAlaThrMetSerThrAlaAlaSerGlyThrThrMetGlyLeuValGluGln 340  
 Db 948 ----- 948  
 QY 341 AlaLysSerLeuLeuAsnLysAlaAspGlyValLysProGlnThrAsnSerThrLys 360  
 Db 949 GCCAAGAGTTTCTTGAGAAACCA----- 972  
 QY 361 AsnSerAlaAlaAlaThrSerProLysGlyThrLeuProAlaAlaLeuGluProGln 380  
 Db 972 ----- 972  
 QY 381 ThrThrValIleHisAsnProValAspGlyIleLysGluSerSerAspSerAlaAsnThr 400  
 Db 973 -----GATGGAGTAAAGGAGTCACTGAGAGTTCAAATACA 1008  
 QY 401 ThrIleGluAspGluAspAlaLysAlaArgLysGlnGluIleLysThrThrGluGln 420  
 Db 1009 ACAATTGAGATGAAGATGTGAAGCAGCAGAGAGAGATTAACAAGTCACTGACAA 1068  
 QY 421 LeuIleGluAlaValAsnAsnGlyAspPheGluAlaTyrAla----- 434  
 Db 1069 CTGATCGAAGCTATCAACAATGGGGACTTTGAAGCCTACACAAATAATCTGTGACCCAGGC 1128  
 QY 434 ----- 434  
 Db 1129 CTTACTGCTTTTGAACCTGAAGCTTTGGGTAAATTTAGTGAAGGGATGGATTTTCCCGA 1188  
 QY 435 PheTyrPheGluAsnLeuLeuAlaLysAsnSerLysProIleHisThrThrIleLeuAsn 454  
 Db 1189 TTCTACTTTGAAAATGCTTTGTCCAAAAGCAATAAACCAATCCACACTATTATTCTAAAC 1248  
 QY 455 ProHisValHisValIleGlyGluAspAlaAlaCysIleAlaTyrIleArgLeuThrGln 474  
 Db 1249 CCTCATGTACATCTGTTAGGGGATGATGCGGCTGCATAGCATATATTAGGCTCAGACAG 1308  
 QY 475 TyrIleAspGlyGlnGlyArgProArgThrSerGlnSerGluGluThrArgValTrpHis 494  
 Db 1309 TACATGATGGCAGTGGAAATGCCAAGACAAATGCATCAGAGAGACTCGTGTGTGGCAC 1368

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QY 495 ArgArgAspGlyLysTrpGlnAsnValHisPheHisCysSerGlyAlaProValAlaPro 514
Db 1369 GCGCGGATGGAAGTGGCAGAAATGTCATTTTCATCGCTCGGGGTCCACACAGTACCC 1428
QY 515 LeuGln 516
Db 1429 ATCAAG 1434

RESULT 8
US-09-925-299-210
; Sequence 210, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 210
; LENGTH: 1551
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (760)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1543)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1544)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1545)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1546)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-210

Alignment Scores:
Pred. No.: 6.2le-170 Length: 1551
Score: 1568.00 Matches: 310
Percent Similarity: 80.34% Conservative: 17
Best Local Similarity: 76.17% Mismatches: 14
Query Match: 57.75% Indels: 66
DB: 9 Gaps: 2

US-09-820-790b-2 (1-516) x US-09-925-299-210 (1-1551)

QY 1 MetalArThrValThrCysThrArgPheThrAspGluTrpGlnLeuTyrcLuAspIle 20
Db 489 ATGGCTTCGCCACACCTGCACCAGGTCACGACGAGTATGAAATTCCTACTGCAGAGGCTT 548
QY 21 GlyLysGlyAlaPheSerValValArgCysValLysLeuCysThrGlyHisGluTrp 40
Db 549 GGAAAGGGGCACTTCAGTGGTGAGAGATGTATGAAATTCCTACTGCAGAGATAT 608
QY 41 AlaAlaLysIleLeuAsnThrLysLysLeuSerAlaArgAspHisGlnLysLeuGluArg 60
Db 609 GCTGCCAAATATACACACCAAAAAGCTTCTGCTAGGATCATCAGAAACTAGAAAGA 668
QY 61 GluAlaArgIleCysArgLeuLeuLysHisSerAsnIleValArgLeuHisAspIle 80
Db 669 GAAGCTAGATCTCCGCTCTTTGAAGCACCCCTAATATTGTGGACTTCATGATAGCAT 728

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QY 81 SerGluGluGlyPheHisTyr-LeuValPheAspLeu-ValThrGlyGlyGluLeuPheG 100
Db 729 TCAGAAAGGGCTTTTCACCTACTTTGGTGGTNGATTAAGTTACTGGAGGTGAAGTGTG 788
QY 100 luAspIleValAlaArGgGluTyTySerGluAlaAspAlaSerHisCysIleGlnIle 120
Db 789 AAGACATAGTGGCAGAGAACTACAGTGAAGCTGATGCCAGTCATTCGATTCAGCAGA 848
QY 120 leLeuGluAlaValLeuHisCysHisGlnMetGlyValValHisArgAspLeuLysProG 140
Db 849 TCCTGGAGGCTGTGCTACACTGCCATCAGATGGCGCTGTGCTCCATCGGACCTGAAGCTG 908
QY 140 luAsnLeuLeuLeuAlaSerLysCysLysGlyAlaAlaValLysLeuAlaAspPheGlyL 160
Db 909 AGAATTTCCTTTAGCTAGCAATCCAAAGGAGCAGCTGTGAATTTGGACACTTTGGCT 968
QY 160 euAlaIleGluValGlnGlyAspGlnGlnAlaTrpPheGlyPheAlaGlyThrProGlyT 180
Db 969 TAGCCATAGAAGTTCAAGGGGACCAGCAGCGTGGTTGGTTTTGCTGGCACACTGGAT 1028
QY 180 yrLeuSerProGluValLeuArgLysGluAlaTyrglyLysProValAspIleTrpAlaC 200
Db 1029 ATCTTCTCYCARAAGTTTTACGTAAAGATCCTATGAAAAGCCAGCTGGATATGTGGCAT 1088
QY 200 ysGlyValIleLeuTyrlleLeuLeuValGlyTyTyProPheTrpAspGluAspGlnH 220
Db 1089 GTGGGTGCATCTCTATATTTCTACTTGTGGGTATCCACCTCTGGGATGAACCAAC 1148
QY 220 lsLysLeuTyrglnGlnIleLysAlaGlyAlaTyrglyAspPheProSerProGluTrpAsp 240
Db 1149 ACAGACTCTATCAGCAGATCAAGGCTGGAGCTTATGATTTCCATCACCAGATGGGACA 1208
QY 240 hrValThrProGluAlaLysAsnLeuIleAsnGlnMetLeuThrIleAsnProAlaLysA 260
Db 1209 CGGTGACTCTGAAGCCCAAGACCTCATCAATAAATGCTTACTATCACCTGCCAAAC 1268
QY 260 rgIleThrAlaHisGluAlaLeuLysHisProTyValCysGlnArgSerThrValAlas 280
Db 1269 GCATCACAGCCTCAGAGGCACCTGAAGCACCATGATGATCTGTCAACGTTCTACTGTGCTT 1328
QY 280 erMetMetHisArgGlnGlnGluThrValGluCysLeuLysLysPheAsnAlaArgLysL 300
Db 1329 CCATGATGCACAGACAGAGACTGTAGACTGCTTTGAAGAAATTTATGCTAGAGAAAC 1388
QY 300 euLysGlyAlaIleLeuThrMetLeuAlaThrArgAsnPheSerValGlyArgGlnT 320
Db 1389 TAAAGGTGGCCCTCTTGACAACTATGTGGCTACAGAAATTTCTCAGCA----- 1438
QY 320 hrThrAlaProAlaThrMetSerThrAlaAlaSerGlyThrThrMetGlyLeuValGluG 340
Db 1438 ----- 1438
QY 340 InAlaLysSerLeuLeuAsnLysLysAlaAspGlyValLysProGlnThrAsnSerThrL 360
Db 1439 --GCCAAGAGTTGTTGAAGAAACCA----- 1462
QY 360 ysAsnSerAlaAlaAlaThrSerProLysGlyThrLeuProAlaAlaLeuGluProG 380
Db 1462 ----- 1462
QY 380 InThrThrValIleHisAsnProValAspGlyIleLysGluSerSerAspSerAlaAsnT 400
Db 1463 -----GATGGAGTAAAGGAGTCAACTGAGAGTTCAAATA 1496
QY 400 hrThrIleGluAspGlu 405
Db 1497 CAACAATTTGAGGATGAA 1513

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## RESULT 9

US-925-299-210  
; Sequence 210, Application US/09925299  
; Publication No. US20030040617A9  
; GENERAL INFORMATION:

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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 210
; LENGTH: 1551
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (760)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1543)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1544)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1545)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1546)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-925-299-210

```

## Alignment Scores:

```

Pred. No.:      6,21e-170      Length:      1551
Score:          1568.00      Matches:      310
Percent Similarity: 80.34%      Conservative: 17
Best Local Similarity: 76.17%      Mismatches: 14
Query Match:      57.75%      Indels:      66
DB:              11          Gaps:      2

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US-09-820-790b-2 (1-516) x US-09-925-299-210 (1-1551)

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QY      1  MetAlaThrThrValThrCysThrArgPheThrAspLysrGlnLeuTyrGluAspIle 20
DB      489  ATGGCTTCGACCAACCTGTCACCGAGTTCACGAGCATATCAGCTTTCCGAGGACTT 548
QY      21  GlyLysGlyAlaPheSerValValArgCysValLysLeuCysThrGlyHisGluTyr 40
DB      549  GGAAAGGGGGCATCTTCAGTGGTGAGAGATGTATGAAATTCCTACTGGACAAAGATAT 608
QY      41  AlaAlaLysIleIleAsnThrLysLysLeuSerAlaArgAspHisGlnLysLeuGluArg 60
DB      609  GTGCGCAAAATATACACCAACCAAAAGCTTCTCTAGGAGATCATCAAGAACTAGAAGA 668
QY      61  GluAlaArgIleCysArgLeuLeuLysHisSerAsnIleValArgLeuHisAspSerIle 80
DB      669  GAAGCTAGACTCCGCTCTTTGAGCACCCCTATATATGCGACTTCATGATAGACATA 728
QY      81  SerGluGluGlyPheHisTyr-LeuValPheAspLeu-ValThrGlyGlyGluLeuPheG 100
DB      729  TCAGAAGAGGGCTTCACTACTTGTGTTNGATTAAAGTTACTGGAGGTGAAGCTGTTG 788
QY      100  LuAspIleValAlaArgGluTyrTyrSerGluAlaAspAlaSerHisCysIleGlnGlnI 120
DB      789  AGACATAGTGGCAAGAGATACTACGTAGAGCTGATGCCAGTCATTCATTCAGCAGA 848
QY      120  IeLeuGlnAlaValLeuHisCysHisGlnMetGlyValValHisArgAspLeuLysProG 140
DB      849  TCTCGAGGCTGCTACACTGCCATCAGATGGCGGTGTCCTCGGACCTGAAGCCTG 908
QY      140  LuAsnLeuLeuLeuAlaSerLysCysLysGlyAlaAlaValLysLeuAlaAspPheGlyL 160

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DB      909  AGAATTTGCTTTTACCTAGCAAAATCCAAAGGGAGCAGCTGTGAATTTGGCAGACTTGGCT 968
QY      160  euAlaIleGluValGlnGlnAspGlnAlaTyrPheGlyPheAlaGlyThrProGlyT 180
DB      969  TAGCCATAGAGCTTCAAGGGGACCAGCAGCGCTGGTTGGTTTGGCTGGCACCACCTGGAT 1028
QY      180  yrLeuSerProGluValLeuArgLysGluAlaTyrGlyLysProValAspIleTtPalac 200
DB      1029  ATCTTTCTTCARAGTTTTACGTAAAGATCCCTTATGGAAGCCAGCTGGATATGTGGGAT 1088
QY      200  ysglyValIleLeuTyrIleLeuValGlyTyrProPheThrAspGluAspGlnH 220
DB      1089  GTGGTGTCTATCTCTATATTTCTACTTGTGGGTATCCACCCCTCTGGGATGAAGACCAAC 1148
QY      220  isLysLeuTyrGlnGlnIleLysAlaGlyAlaTyrAspPheProSerProGluTtPaspT 240
DB      1149  ACAGACTCTATCAGCAGATCAGGCTGAGCTTATGATTTTCCATCACCAGATGGGACA 1208
QY      240  hrValThrProGluAlaLysAsnLeuIleAsnGlnMetLeuThrIleAsnProAlaLysA 260
DB      1209  CGGTGACTCTCGAGCCCAAGACCTCATCAATAAATGCTTACTATCAACCCCTGCCAAC 1268
QY      260  rgIleThrAlaHisGluAlaLeuLysHisProTrrPValCysGlnArgSerThrValAla 280
DB      1269  GCATCAGCCTTCAGAGGCACTGAAGCACCATGGATCTGTCAACGTTCTACTGTGCTT 1328
QY      280  erMetMetHisArgGlnGlnThrValGluCysLysLysPheAsnAlaAtGtGlySL 300
DB      1329  CCATGATGCACAGCAGGAGCTGTAGCTGCTTGAAGAAATTTAATGCTAAGAAGAAC 1388
QY      300  euLysGlyAlaIleLeuThrThrMetLeuAlaThrArgAsnPheSerValGlyA-rgLnt 320
DB      1389  TAAAGGTGCCATCTTGACAACTATGCTGCTACAGGAATTTCTCAGCA- 1438
QY      320  hrThrAlaProAlaThrMetSerThrAlaAlaSerGlyThrThrMetGlyLeuValGlu 340
DB      1438  ----- 1438
QY      340  lnAlaLysSerLeuLeuAsnLysLysAlaAspGlyValLysProGlnThrAsnSerThrL 360
DB      1439  --GCCAAGAGTTTGTGAAGAACCA----- 1462
QY      360  ysAsnSerAlaAlaAlaThrSerProLysGlyThrLeuProProAlaAlaLeuGluProG 380
DB      1462  ----- 1462
QY      380  lnThrValIleHisAsnProValAspGlyIleLysGluSerSerAspSerAlaAsnT 400
DB      1463  -----GATGGAGTAAAGGAGTCAACTGAGAGTCAAAATA 1496
QY      400  hrThrIleGluAspGlu 405
DB      1497  CAACAATTGGAGTAA 1513

```

## RESULT 10

```

US-09-918-995-316
; Sequence 316, Application US/0918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 316
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Homo sapiens

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```
/ ;
; NAME/KEY: misc.feature
; LOCATION: (1)-(474)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-316

Alignment Scores:
Pred. No.: 5,47e-73 Length: 474
Score: 718.00 Matches: 132
Percent Similarity: 97.14% Conservative: 4
Best local Similarity: 94.29% Mismatches: 4
Query Match: 26.45% Indels: 0
DB: 11 Gaps: 0

US-09-820-790B-2 (1-516) x US-09-918-995-316 (1-474)
QY 162 IleGluValGlnGlyAspGlnGlnAlaTrpPheGlyPheAlaGlyThrProGlyTyrLeu 181
DB 55 ATCGAAGTACAGGAGAGACGACGAGGCTTGTTGGTTTGTGTCGCCACCCAGGTTACTGTG 114
QY 182 SerProGluValLeuAlaGlyLysGluAlaTyrGlyLysProValAspIleTrpAlaCysGly 201
DB 115 TCCTTGGAGCTTGGAGGAAGATCCCTATGGAANAACGTGGGATATCTGGCCCTGCCGG 174
QY 202 ValIleLeuTyrIleLeuLeuValGlyTyrProPheTrpAspGluAspGlnHisLys 221
DB 175 GTATCCCTGTATATCTCTCTGTTGGGCTATCTCTCTCTGGGATGAGGATCAGCACAA 234
QY 222 LeuTyrGlnGlnIleLysAlaGlyAlaTyrAspPheProSerProGluTrpAspThrVal 241
DB 235 CTGTATCAGCAGATCAGGCTGAGGCTATGATTTCCCATCCACAGATGGGACACGTA 294
QY 242 ThrProGluAlaLysAsnLeuIleAsnGlnMetLeuThrIleAsnProAlaLysArgIle 261
DB 295 ACTCTGAAGCCAGAACTTGATACACAGATGCTGACCATTAACCCAGAAAGGCGATC 354
QY 262 ThrAlaHisGluAlaLeuLysHisProTrpValCysGlnArgSerThrValAlaSerMet 281
DB 355 ACGGCTGACCAAGGCTCTCAAGCACCCGTTGGTCTGTCAACGATCCACGCTGGCATC 414
QY 282 MetHisArgGlnGluThrValGluCysLeuLysLysPheAsnAlaArgLysLeuLys 301
DB 415 ATGATCTGTAGGAGACTGTGGAGTGTGGCGAAGTTCAATGCCCGGAGAAACTGAAG 474

RESULT 11
US-10-024-036B-1
; Sequence 1, Application US/10024036B
; Publication No. US20030028004A1
; GENERAL INFORMATION:
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: 68730 and 69112, Protein Kinase
; TITLE OF INVENTION: Molecules and Uses Therefor
; FILE REFERENCE: MPI2000-521PIR(M)
; CURRENT APPLICATION NUMBER: US/10/024, 036B
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/258222
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1772
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)...(168)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (169)...(1242)
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (1243)...(1772)
; FEATURE:

/ ;
; NAME/KEY: unsure
; LOCATION: 1
; OTHER INFORMATION: n may be A, T, G, or C.
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 3
; OTHER INFORMATION: n may be A, T, G, or C.
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 5
; OTHER INFORMATION: n may be A, T, G, or C.
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (6)...(6)
; OTHER INFORMATION: n may be A, T, G, or C.
US-10-024-036B-1

Alignment Scores:
Pred. No.: 8,48e-62 Length: 1772
Score: 628.50 Matches: 167
Percent Similarity: 51.13% Conservative: 82
Best local Similarity: 34.29% Mismatches: 197
Query Match: 23.15% Indels: 41
DB: 14 Gaps: 12

US-09-820-790B-2 (1-516) x US-10-024-036B-1 (1-1772)
QY 14 TyrGlnLeuTyrGluAspIleGlyLysGlyAlaPheSerValValAlaArgCysVallys 33
DB 235 TTCGAGTTCAAAGAGAGACCCCGAACCGGGCGCTTTTCGAAAGTGGTTTTAGCTGAAGAG 294
QY 34 LeuCysThrGlyHisGluTyrAlaAlaLysIleLeuAsnThrLysLysLeuSerAlaArg 53
DB 295 AAGGCAACTGCGACGCTCTTGTCTGTAAGTGTATCCCTAGAGAGCGCTGAGGGCGAAG 354
QY 54 AspHisGlnLysLeuGluArgGluAlaArgIleCysArgLeuLeuLysHisSerAsnIle 73
DB 355 GAA---AGCAGCATAGAGAATGAGATGACGCTCTGAGAAAGATTAAAGCATGAAATATT 411
QY 74 ValArgLeuHisAspSerIleSerGluGluGlyPheHisTyrLeuValPheAspLeuVal 93
DB 412 GTTGCCCTGGAGAGACTTTATGAAGCCCAATACCTGTACTTGTGTCATGCGAGCTGGTG 471
QY 94 ThrGlyGlyGluLeuPheGluAspIleValAlaArgGluTyrTrpSerGluAlaAspAla 113
DB 472 TCGGCTGGAGAGCTGTTTGACCGATAGTGGAGAGAGGCTTTATACAGAGAGATGCC 531
QY 114 SerHisCysIleGlnIleLeuGluAlaValLeuHisCysHisGlnMetGlyValVal 133
DB 532 AGCACTCTGATCCGCCAAGTCTTGGAGCGCTGTACTATCTCCACAGAAATGGGCATCGTC 591
QY 134 HisArgAspLeuLysProGluAsnLeuLeuAlaSerLysCysLysGlyAlaAlaVal 153
DB 592 CACAGAGACCTCAAGCCCGGAAATCTCTGTACTACAGTCAAGATGAGGAGTCCAAATA 651
QY 154 LysLeuAlaAspPheGlyLeuAlaIleGluValGlnGlyAspGlnGlnAlaTrpPheGly 173
DB 652 ATGATCAGTACTTGGATTGTCA---AAAATGAGGCGCAAGAGATGTGTATGTCCTACT 708
QY 174 PheAlaGlyThrProGlyTyrLeuSerProGluValLeuArgLysGluAlaTyrGlyLys 193
DB 709 GCCTGTGGAACCTCCAGGCTATGCTGCTCGCTGAACTCTCGCCAGAACCTTACAGCAA 768
QY 194 ProValAspIleTrpAlaCysGlyValIleLeuTyrIleLeuValGlyTyrProPro 213
DB 769 GCGCTGTACTCTGCTCCATCGAGTATGCTGCTACTCTGTCTGCGGCTACCTCCT 828
QY 214 PheTrpAspGluAspGlnHisLysLeuTyrGlnGlnIleLysAlaGlyAlaTyrAspPhe 233
DB 829 TTTTATGATGAAATGACTCCAGCTCTTTGAGCAGATCTCTCAAGCGGCAATATGAGTT 888
QY 234 ProSerProGluTrpAspThrValThrProGluAlaLysAsnLeuIleAsnGlnMetLeu 253
```

Db 889 GACTCTCCCTACTGGGATGACATCTCCGACTCTGCAAAAGACTTCATTCGGAACCTGATG 948  
 QY 254 ThrIleasnProAlaLysArgIleThrAlaHisGluAlaLeuLysHisProTrpValCys 273  
 Db 949 GAGAGACCCCGAATAAAGATACACCTGTGACGACGCGATCCGCGACCCCATCGATCGGT 1008  
 QY 274 GlnArgSerThrValAlaSerMetMetHisArgGlnGluThrValGluCysLeuLys 293  
 Db 1009 GGTGACACACCCCTCAACAAAACATCCAGGCTCCGTCAGGCCGACGATCCGGAACAC 1068  
 QY 294 PheAsnAlaArgGlyLeuLysGlyAlaIleLeuThrMetLeuAla-----Thr 311  
 Db 1069 TTT---GCCAAGACCAATGGAGCAAGCACTTTAATGCCAGCGCGCTGAGACATATG 1125  
 QY 312 ArgAsnPheserValGlyArgGlnThrThrAlaProAlaThrMetSerThrAlaAlaSer 331  
 Db 1126 AGAAACTACACTCGGACGAGCTGGACAGT-----TCAATGCAAGTGT 1173  
 QY 332 GlyThrMetGlyLeuValGluGlnAlaLysSerLeuLeuAsnLysLysAlaAspGly 351  
 Db 1174 TCGAGCAGCTCAGTGTGGCCAGCCAAAAGACTGT-----GGTATGTA 1218  
 QY 352 ValIysProGlnThrAsnSerThrLysAsnSerAlaAlaAlaThrSerProLysGlyThr 371  
 Db 1219 GCAAAACCAAGATCCCTCAGCTCAGACTGAAGACGAGCTGGGTGGAGGAGGAGCC 1278  
 QY 372 -----LeuProAlaAlaLeuGluProGlnThrThrValIleHisAsnPro 387  
 Db 1279 GGCATCTGCCGAGCCTCCGTGTC-----CAGCGCTTCTTACTACTATCC 1329  
 QY 388 ValAspGlyIleLysGluSerSerAspSerAlaAsnThrIleGluAspGluAspAla 407  
 Db 1330 ATG-----TCATGGGACCC-----AGGACTTTTATTAACATGTAATCA 1368  
 QY 408 LysAlaArgLysGlnGluIleLysThrThrGluGlnLeuLeuAlaValAsnAsn 427  
 Db 1369 CTGGCGGGTGCAGTGGCTCACCGCTGTAATCCCAACACTTGGAGGCTGGAGCAGA 1428  
 QY 428 GlyAspPheGluAlaTyrAlaPheTyrPheGluAsnLeuLeuAlaLysAsnSerLysPro 447  
 Db 1429 GGACTGTTTGAGTTCAGGAGTTT-----AAGACC 1458  
 QY 448 IleHisThrThrIleLeuAsnProHisValHis-ValIleGlyGluAspAlaAlaCys-I 467  
 Db 1459 AGCCTGCCAACATGCTGAACCCCATCTCTACTAAATATAAAATTAGCCGGGTGG 1518  
 QY 467 leaLaryIleArgLeuThrGlnTyrIleAspGlyGlnGlyArgProArgThrSerGlnS 487  
 Db 1519 TGGCGAGCACCTGTAATGTCAGCTACTTGGAGGCTGAGGCAGG---AGATCACTTGAA 1575  
 QY 487 erGluGlnThrArgVal 492  
 Db 1576 CCCAGGAAGCGGAGT 1592

## RESULT 12

US-10-355-975-3

; Sequence 3, Application US/10355975

; Publication No. US20030162277A1

; GENERAL INFORMATION:

; APPLICANT: Immunex Corporation

; APPLICANT: Bird, Timothy A.

; APPLICANT: Virca, G. Duke

; APPLICANT: Martin, Unja

; APPLICANT: Anderson, Dirk M.

; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES

; FILE REFERENCE: 2923-A

; CURRENT APPLICATION NUMBER: US/10/355,975

; CURRENT FILING DATE: 2003-01-30

; PRIOR FILING DATE: 2000-05-26

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 1694

; TYPE: DNA

; ORGANISM: Mus musculus

US-10-355-975-3

## Alignment Scores:

Pred. No.: 8,56e-61 Length: 1694  
 Score: 619.50 Matches: 131  
 Percent Similarity: 58.13% Conservative: 62  
 Best Local Similarity: 39.46% Mismatches: 124  
 Query Match: 22.82% Indels: 15  
 DB: 12 Gaps: 5

US-09-820-790B-2 (1-516) x US-10-355-975-3 (1-1694)

QY 14 TyrGlnLeuTyrGluAspIleGlyLysGlyAlaPheSerValValArgCysValLys 33  
 Db 309 TTCGAGTTCARAGAGACACCTCGGAACCTGGGGCTTTCTGAAGTTGTTTGGCGGAGGAG 368  
 QY 34 LeuCysThrGlyHisGluTyrAlaAlaLysIleIleAsnThrLysLysLeuSerAlaArg 53  
 Db 369 AAAGCTACTGGGAAGCTCTTCGAGTGAAGTCATCCCGAAGAGCGCTGAAGGCGAAG 428  
 QY 54 AspHisGlnLysLeuGluArgGluAlaArgIleCysArgLeuLeuLysHisSerAsnIle 73  
 Db 429 GAG---AGCAGCATCGAGACGAGATTGCCGTCTTAGAAGATTAAAGCATGAACACATT 485  
 QY 74 ValArgLeuHisAspSerIleSerGluGluGlyPheHisTyrLeuValPheAspLeuVal 93  
 Db 486 GTTGCCTTGGAGATATTTATGAAGCCCAATCACTCTACCTGGTCAATGCAACTGTG 545  
 QY 94 ThrGlyGlyGluLeuPheGluAspIleValAlaArgGluTyrTyrSerGluAlaAspAla 113  
 Db 546 TCTGTGGAGAACTCTTCGATCGGATAGTGGAGAGGGGTTTACACAGAGAAAGATGCC 605  
 QY 114 SerHisCysIleGlnGluIleGluAlaValLeuHisCysHisGlnMetGlyValVal 133  
 Db 606 AGACATCTCATCCGCGAGTCTCGATGCGGTATATCTTACAGTCAAGAGGAGGATGTC 665  
 QY 134 HisArgAspLeuLysProGluAsnLeuLeuAlaSerCysLysGlyAlaAlaVal 153  
 Db 666 CACAGGAGCTCAAGCCGGAATCTCTTATACAGTCAAGAGGAGGAGTCCAAATA 725  
 QY 154 LysLeuAlaAspPheGlyLeuAlaIleGluValGlnGlyAspGlnGlnAlaTrpPheGly 173  
 Db 726 ATGATCAGTCACTTTGGCTTGTGCG---AAAATGGAGGCAAGGAGATGTGATGCCAAG 782  
 QY 174 PheAlaGlyThrProGlyTyrLeuSerProGluValIleArgLysGluAlaTyrGlyLys 193  
 Db 783 GCCTGGGAGACCCAGGCTATGTTGCTCCGGAAGTTCGCCCGCAAAACCGTACACAA 842  
 QY 194 ProValAspIleTrpAlaCysGlyValIleLeuTyrIleLeuLeuValGlyTyrPro 213  
 Db 843 GCTGTGGACTGTGTGTCATCGGGTGATCGCTATATCTTGTCTGTGTTACCTCTCT 902  
 QY 214 PheTrpAspLysGlnHisLysLeuTyrGlnGlnIleLysAlaGlyAlaTyrAspPhe 233  
 Db 903 TTTTATGATGAATAATGACTCGAAGCTGTTTGAACAGATCTCTCAAGGCGAAGATATGATTT 962  
 QY 234 ProSerProGluTrpAspThrValThrProGluAlaLysAsnLeuIleAsnGlnMetLeu 253  
 Db 963 GATTCCTCTACTGGGATGACATCTCCGACTCTGCGAAGAGATCTCATTCGGAATCTGATG 1022  
 QY 254 ThrIleasnProAlaLysArgIleThrAlaHisGluAlaLeuLysHisProTrpValCys 273  
 Db 1023 GAGAAGACCCCAATAAAGATACACTTGTGACGACGAGCTCGACACCCCATGGATGCT 1082  
 QY 274 GlnArgSerThrValAlaSerMetMetHisArgGlnGluThrValGluCysLeuLysLys 293  
 Db 1083 GGTGACACAGCCCTTAGCAAAAACATTCACGAATCTGTGAGTGCCAGATCCGGAAGAT 1142  
 QY 294 -----PheAsnAlaArg-----ArgLysLeuLys 301

```
Db 1143 TTTGCAAGACAAATGGAGACAAGCGTTTAAAGCCAGCGCAGTCGTGAGACATATGCGG 1202
QY 302 GlyAlaIleLeuThrThrMetLeuAlaThrArgAsnPheSerValGlyArgGlnThrThr 321
Db 1203 AGGCTCCAGCTTGGCAGCAGCTGGAGACATTCAATGCAAGTGTCTCAAGCAACCTCAGT 1262
QY 322 AlaProAlaThrMetSerThrAlaAlaSerGlyThr 333
Db 1263 TTG---GCCACCCAAAAGATGTGCGTCTGGCACC 1295

RESULT 13
US-09-764-868-184
; Sequence 184, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 184
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (427)
; OTHER INFORMATION: n equals a.t.g, or c
US-09-764-868-184
```

```
Alignment Scores:
Pred. No.: 1,33e-61 Length: 435
Score: 618.50 Matches: 127
Percent Similarity: 91.49% Conservative: 2
Best Local Similarity: 90.07% Mismatches: 9
Query Match: 22.78% Indels: 3
DB: 10 Gaps: 1
```

US-09-820-790B-2 (1-516) x US-09-764-868-184 (1-435)

```
QY 39 GluTyrAlaAlaLysIleLeuAsnThrLysLysLeuSerAlaArgAspHisGlnLysLeu 58
Db 13 GAATATGTCGCCAAATATATACACACCAAAAGCTTCTGCTAGGATCATCAGAACTA 72
QY 59 GluArgGluAlaArgIleCysArgLeuLeuLysHisSerAsnIleValArgLeuHisAsp 78
Db 73 GAAAGAGAGCTAGAAATCTGCCGCTTTTGAAGCACCCCTAATATTGTGCACTTCATGAT 132
QY 79 SerIleSerGluGluGlyPheHisTyrLeuValPheAspLeuValThrGlyGlyGluLeu 98
Db 133 ACATATATCAGAGAGGCGTTTCACTACTTGTGTGTTGATTAGTTACTGAGGTGAATG 192
QY 99 PheGluAspIleValAlaArgGluTyrTyrSerGluAlaAspAlaSerHisCysIleGln 118
Db 193 TTTGAAGACATAGTGGCAAGAGAAATACATACAGTCAAGCTGATGCCAGTCATTGTATACAG 252
QY 119 GlnIleLeuGluAlaValLeuHisCysHisGlnMetGlyValValHisArgAspLeuLys 138
Db 253 CAGATTCTAGAAAGTGTAAATCATTTGCACCTTAATGGCATAGTTTCACAGGGACCTGAAG 312
QY 139 ProGlu-AsnLeuLeuAlaSerLysCysLysGlyValAlaAlaValLysLeu-AlaAsp 158
Db 313 CTGAGGAAATTTGTTTACAGCAATCCAGGGAGCAGCTGTGAATTTGGCAGACT 372
QY 158 heGlyLeuAlaIleGlnValGlnGlyAspGlnGlnAlaIlePheGlyPheAlaGly 176
Db 373 TTGGSTTGGCCATAGAAGTTCAAGGGGACCAGCCAGCGTGGGTTTGTGTTGGG 431

RESULT 14
US-09-835-788A-6
```

```
; Sequence 6, Application US/09835788A
; Patent No. US20020077458A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Death Domain-Containing Receptor Polynucleotides, Polypeptid
; FILE REFERENCE: PT018P1
; CURRENT APPLICATION NUMBER: US/09/835,788A
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: PCT/US00/28666
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/159,585
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 60/167,246
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1578
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-835-788A-6

Alignment Scores:
Pred. No.: 1.14e-60 Length: 1578
Score: 618.00 Matches: 135
Percent Similarity: 56.94% Conservative: 66
Best Local Similarity: 38.24% Mismatches: 134
Query Match: 22.76% Indels: 18
DB: 9 Gaps: 6

US-09-820-790B-2 (1-516) x US-09-835-788A-6 (1-1578)
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QY 14 TyrGlnLeuTyrGluAspIleGlyLysGlyAlaPheSerValValArgCysValLys 33
Db 63 TTCGAGTTCAAAAGAGACCCCTCGAACCGGGCGCTTTCCGAAGTGTGTTTAGCTGAAGAG 122
QY 34 LeuCysThrGlyHisGluTyrAlaAlaLysIleLeuAsnThrLysLysLeuSerAlaArg 53
Db 123 AAGGCAACTGCCAAGCTCTTTGCTGAGTGTATCCCTAAGAGCGCTGAGGGCGAAG 182
QY 54 AspHisGlnLysLeuGluArgGluAlaArgIleCysArgLeuLeuLysHisSerAsnIle 73
Db 183 GAA---AGCAGCATAGAGATGAGATAGCGCTCTGAGAAAGATTAAAGCATGAAATATT 239
QY 74 ValArgLeuHisAspSerIleSerGluGlnGlyPheHisTyrLeuValPheAspLeuVal 93
Db 240 GTTGCCCTGGGAAGACATTTATGAAAGCCCAATCACTGTACTGTGTGTGTCATGCGCTGTG 299
QY 94 ThrGlyGlyGluLeuPheGluAspIleValAlaArgGluTyrTyrSerGluAlaAspAla 113
Db 300 TCCGCTGGAGAGCTGTTGACCGGATAGTGGAGAGGGGTTTATACAGAGAAGATGCC 359
QY 114 SerHisCysIleGlnGlnIleLeuGluAlaValLeuHisCysHisGlnMetGlyValVal 133
Db 360 AGCACTCTGATCCGCCAAGTCTTGGACGCCGTGACTACTCTCCACAGAAATGGGATGCTC 419
QY 134 HisArgAspLeuLysProGluAsnLeuLeuAlaSerLysCysLysGlyValAlaAlaVal 153
Db 420 CACAGAGACCTCAAGCCCCGAAATCTTTGTACTACATGATGAGATGGAGGTCCAAATA 479
QY 154 LysLeuAlaAspPheGlyLeuAlaIleGluValGlnGlyAspGlnGlnAlaIlePheGly 173
Db 480 ATGATCATGACTTTGGATTGTCA---AAATGGAGGGCAAGAGATGTGATGTGCCACT 536
QY 174 PheAlaGlyThrProGlyTyrLeuSerProGluValLeuArgLysGluAlaIlePheGlyLys 193
Db 537 GCCTGTGGAATCCAGGCTATGTCTGCTGAGTCTCTGCCAGAAACCTTACAGAAA 596
QY 194 ProValAspIleThrPalCysGlyValIleLeuTyrIleLeuValGlyTyrProPro 213
Db 597 GCGGTGTACTGCTGCTCCATCGGAGTGTATGCCATATCTTGTCTGTGCGGCTACCCCTCCT 656
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QY		214	PheThrPaspGluAspGlnHisLysLeuTryGlnGlnIleLysAlaGlyAlaTryraspPhe	233
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QY		234	ProSerProGluTrApSthrValThrProGluAlaLysAsnLeuIleAsnGlnMetLeu	253
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QY		322	AlaProAlaThrMetSerThrAlaAlaSerGlyThrThrMetGlyLeuValGluGlnAla	341
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QY		342	LysSerLeuLeuAsnLysLysAlaAspGlyValLysPro	354
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Db		1065	TCATTCTCTTCGTCGGGGGGCTCTCAGGAGTGTGGAGCG	1103

Qy	34	LeuCysThrGlyHisClutryAlaalaLlelleAsnThrLysLysLeuSerAlaArg	53
Db	123	AAGCAACTGGCAAGCTTCCTTGCCTGAAGGTATCCCTAAAGAAGCGCTGAGGACG	182
Qy	54	AspHisGlnLysLeuGluArgGluAlaArlleCysArgLeuLeuLysHisSerAsnIle	73
Db	183	GAA--AGCAGCATAGAGAAATGAGTAGCGCTCTGAGAAAGATTAGCATGAAATATT	239
Qy	74	ValArgLeuHisAspSerIleSerGluGluGlyPheHisTyrrLeuValPheAspLeuVal	93
Db	240	GTTCCCTCGAAGACATTTATGAAGACCCCAAAATCAACCTGTACTTGTCATCGACGTGGT	299
Qy	94	ThrGlyGlyLeuLeuPheGluAspIleValAlaArgGluTyrrTyrrSerGluAlaAspAla	113
Db	300	TCCGCTGGAGAGCTGTTTGACCGGATAGTGGAGAGGGGTTTTATACAGAGAAGATGCC	359
Qy	114	SerHisCysIleGlnIleLeuGluAlaValLeuHisCysHisGlnMetGlyValVal	133
Db	360	ASCACCTCGATCGGCACAAGCTCTGGAGCCCGGTACTACTCTCCACAGAATGGCACATCCTC	419
Qy	134	HisArgAspLeuLysProGluAsnLeuLeuAlaSerLysCysLysGlyAlaAlaVal	153
Db	420	CACAGAGACCTCAAGCCGAAAAATCTCTTGTACTACAGTCAAGATGAGGAGTCCAAAATA	479
Qy	154	LysLeualaaspPheGlyLeualaIleclValGlnGlyAspGlnGlnAlatrppHegly	173
Db	480	ATGATCATGTAAGTTCGGATTGTCA---AAATCGAGGCGCAAAGGAGATGTGATGCCACT	536
Qy	174	PheAlaGlyThrProGlyTyrrLeuSerProGluValLeuArgGlyAlaTrGlyLys	193
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Qy	194	ProValaspileThralacCysGlyValleuTyrrIleLeuLeuValGlyTyrrProPro	213
Db	597	GCGCTGACTGCTGGTCCAACCTCGGATGATTCCTACATCTTGCCTCGGCTACCCTCT	656
Qy	214	PheTrpAspGluaspGlnHisLysLeutyrrGlnGlnIleLysAlaGlyAlaTyrrAspPhe	233
Db	657	TTTATGATGAATGACTCCAAGCTCTTTGACGACATCTCTCAAGGCGGAATATGATGTTT	716
Qy	234	ProSerProGluTrpAspThrValThrProGluAlaLysAsnLeuLeuAsnGlnMetLeu	253
Db	717	GACTCTCCCTACTGGATGACATCCGACTCTGCAAAAGACTTCATTCGGAACCTGTATG	776
Qy	254	ThrIleasnProAlatylsArgIleThrAlaHisGluAlaLeuLysHisProtyrrValCys	273
Db	777	GAGAGGACCCGHAFAAAGATACACGTGTGACGAGCAGCTCGSCACCCATGGATCGCT	836
Qy	274	GlnArgSerThrValalaserMetMetHisArgGlnGlnThrValGluCysLeuLysLys	293
Db	837	GGTGACACAGCCCTCAACAAAACATCCACGAGTCGCTCAGCGCCGACCCGGAACAAAC	896
Qy	294	-----PheAsnAlaArg-----ArgLysLeuLys	301
Db	897	TTTGCCAGCAAAATGGAGCAAGCATTTAATGCCACGGCGCTCGTGAGACATATGAGA	956
Qy	302	GlyAlaIleLeuThrThrMetLeuAlaThrArgAsnPheSerValGlyArgGlnThrThr	321
Db	957	AAACTACACTTCGGCAGCAGCTGGACAGCTCAAAATGCAAGTGTTCG---AGCAGCCCTC	1013
Qy	322	AlaProAlaThrMetSerThrAlaAlaSerGlyThrThrMetGlyLeuValGluGlnAla	341
Db	1014	AGTTTGGCCACCCAAAAGACTGTGCGCTGCGCACTTCCACGCTCTGTTT-----	1064
Qy	342	LysSerLeuLeuasnLysLysAlaSpGlyValLysPro	354
Db	1065	TCATTCTTCTTCGTGGGGTCTCAGAGTGTGAGCCG	1103



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 10, 2003, 04:14:34 ; Search time 83 Seconds  
(without alignments)

986.782 Million cell updates/sec

Title: US-09-820-790b-2

Perfect score: 2715

Sequence: 1 MATVTCTRTFTDEQLYEDL.....DGKQNVHFCGAPVAPLQ 516

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq.19Jun03.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2715	100.0	516	AAE30198	Human kinase prote
2	2692	99.2	542	ABP70158	Amino acid sequenc
3	2476.5	91.2	641	AA166791	Amino acid sequenc
4	2445.5	90.1	503	AA168786	Amino acid sequenc
5	2241	82.5	588	AAEL6276	Human kinase PKIN
6	2230	82.1	525	AA179441	Human protein SEQ
7	2230	82.1	525	AA179441	Human protein sequ
8	2225.5	82.0	565	AAE24635	Human calcium/cal
9	2225.5	82.0	565	ABG75873	Novel human kinase

10	2222	81.8	518	22	AAW78457	Human protein SEQ
11	2070	76.2	499	22	AAU03512	Human protein kina
12	2070	76.2	499	24	ABR41267	Human DITFP intrac
13	2067	76.1	605	22	ABG16826	Novel human diagno
14	1872	69.0	493	22	AB565515	Drosophila melanog
15	1872	69.0	493	22	AB566655	Drosophila melanog
16	1872	69.0	493	22	AB566656	Drosophila melanog
17	1775.5	65.4	461	24	ABP96055	Human protein kina
18	1544.5	56.9	372	22	AAU87358	Novel central nerv
19	1405	51.7	264	20	AAV43920	Rat protein kinase
20	1326	48.8	369	24	ABP96056	Human protein kina
21	1294	47.7	264	20	AAV43919	Rat protein kinase
22	1270.5	46.8	469	24	ABP96084	Human protein kina
23	1174	43.2	261	21	AB534443	Human colon cancer
24	1138	41.9	282	21	AAV68777	Amino acid sequenc
25	860.5	31.7	236	22	ABG20751	Novel human diagno
26	805.5	29.7	290	22	AAW25290	Human protein sequ
27	630	23.2	502	21	AAV54580	A rat calcium/cal
28	619.5	22.8	284	22	AB315059	Human nervous syst
29	619.5	22.8	355	22	AA550055	Murine Dendritic C
30	617.5	22.7	355	23	AB508178	Human Cam kinase I
31	616.5	22.7	355	22	AAE11777	Human kinase (PKIN
32	616.5	22.7	355	22	AAW41268	Human polypeptide
33	616.5	22.7	385	22	AAW39482	Human polypeptide
34	616.5	22.7	385	22	AAW39482	Amino acid sequenc
35	613.5	22.6	357	22	AAE11768	Human kinase (PKIN
36	610.5	22.5	450	22	AB568144	Drosophila melanog
37	609.5	22.4	357	22	AAU03508	Human protein kina
38	607	22.4	356	22	AA584360	Amino acid sequenc
39	605.5	22.3	405	22	AB58176	Drosophila melanog
40	593	21.8	257	23	AAW49425	Human serine/threo
41	585.5	21.6	389	21	AAV68793	Amino acid sequenc
42	584.5	21.5	460	23	AB569792	Human CAPPKL polyp
43	584.5	21.5	476	23	AB569793	Human CAPPKL polyp
44	584.5	21.5	476	23	AA522764	Human calmodulin k
45	584.5	21.5	497	22	AAW41547	Human polypeptide

#### ALIGNMENTS

RESULT 1  
AAE30198  
ID AAE30198 standard; Protein; 516 AA.

XX AC AAE30198;

XX DT 24-FEB-2003 (first entry)

XX DE Human kinase protein.

XX KW Human; calcium/calmodulin-dependent protein kinase; immune response;

XX KW drug screening; carcinoma; inflammation; immune disorder; gene therapy;

XX KW growth disorder; developmental disorder; chromosome 7.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 9..17 /note= "Tyrosine kinase phosphorylation site"

FT Region 20..43 /note= "Protein kinase C phosphorylation site"

FT Modified-site 36..39 /note= "Casein kinase II phosphorylation site"

FT Modified-site 47..49 /note= "Protein kinase C phosphorylation site"

FT Modified-site 48..51 /note= "cAMP and cGMP-dependent protein kinase phosphorylation site"

FT Modified-site 51..54 /note= "Casein kinase II phosphorylation site"

FT Modified-site 51..53 /note= "Protein kinase C phosphorylation site"

FT

FT Modified-site 79..82 /note= "Casein kinase II phosphorylation site"  
 FT Modified-site 94..97 /note= "Casein kinase II phosphorylation site"  
 FT Modified-site 102..112 /note= "Casein kinase II phosphorylation site"  
 FT Region 132..144 /note= "Serine/Threonine protein kinase active-site signature"  
 FT Region 195..215 /note= "Helix 1"  
 FT Modified-site 259..262 /note= "cAMP and cGMP-dependent protein kinase phosphorylation site"  
 FT Modified-site 262..265 /note= "Casein kinase II phosphorylation site"  
 FT Modified-site 302..307 /note= "N-myristoylation site"  
 FT Modified-site 313..316 /note= "N-glycosylation site"  
 FT Region 319..339 /note= "Helix 2"  
 FT Modified-site 332..337 /note= "N-myristoylation site"  
 FT Modified-site 357..360 /note= "N-glycosylation site"  
 FT Modified-site 358..360 /note= "Protein kinase C phosphorylation site"  
 FT Modified-site 367..369 /note= "Protein kinase C phosphorylation site"  
 FT Modified-site 390..395 /note= "N-myristoylation site"  
 FT Modified-site 399..402 /note= "N-glycosylation site"  
 FT Modified-site 400..403 /note= "Casein kinase II phosphorylation site"  
 FT Modified-site 401..404 /note= "Casein kinase II phosphorylation site"  
 FT Modified-site 485..488 /note= "Casein kinase II phosphorylation site"  
 FT W0200279431-A2.  
 PN 10-OCT-2002.  
 PD 01-APR-2002; 2002WO-US09744.  
 PE 30-MAR-2001; 2001US-0820790.  
 PR (PEKE ) PE CORP NY.  
 PA (BEAS/) BEASLEY E M.  
 XX Shao W, Merkulov GV, Di Francesco V;  
 XX WPI; 2003-046806/04.  
 XX N-PSDB; AAD47686.  
 XX New peptides related to calcium/calmodulin-dependent protein kinase  
 PT subfamily useful for treating disorders associated with abnormal  
 PT expression of kinase in fetal brain, testis, lung small cell carcinoma,  
 PT uterus adenocarcinoma  
 XX Claim 1; Fig 2A; 86pp; English.  
 XX The invention relates to new peptides related to calcium/calmodulin-  
 CC dependent protein kinase subfamily. The peptides are useful in  
 CC substantial and specific assays related to functional information of the  
 CC peptide sequences, to raise antibodies or to elicit immune response, as  
 CC reagents in assays to determine the levels of protein in biological  
 CC fluids and as markers for tissues where the corresponding protein is  
 CC expressed. The peptides and antibodies are useful in drug screening  
 CC assays, tissue typing and pharmacogenomic analysis. They are also useful  
 CC in treating disorders associated with the absence of, inappropriate or

CC unwanted expression of kinase protein in fetal brain, testis, lung small  
 CC cell carcinoma or uterus endometrium adenocarcinoma, such as cancer,  
 CC inflammation, immune disorders or disorders affecting growth and  
 CC development. The invention is useful as models for the development of  
 CC human therapeutic targets, aid in the identification of therapeutic  
 CC proteins and serve as targets for the development of human therapeutic  
 CC agents that modulate kinase activity in cells and tissues that express  
 CC the transporter. The host cells are useful in producing a kinase protein  
 CC or peptide and non-human transgenic animals. The invention is useful in  
 CC gene therapy. Kinase protein gene is located on chromosome 7. The present  
 CC sequence is human kinase protein.  
 XX  
 SQ Sequence 516 AA;  
 Query Match 100.0%; Score 2715; DB 24; Length 516;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-251;  
 Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MATVTCTRTDEYQLYEDIGKGFVVRVCVKLCTGHEVAAKIINTKLSARDHOKLER 60  
 DB 1 MATVTCTRTDEYQLYEDIGKGFVVRVCVKLCTGHEVAAKIINTKLSARDHOKLER 60  
 QY 61 EARICRLKHSNIVRLHDSISEGPHYLVDLVLTGGELFEDIVAREYISEADASHCICQI 120  
 DB 61 EARICRLKHSNIVRLHDSISEGPHYLVDLVLTGGELFEDIVAREYISEADASHCICQI 120  
 QY 121 LEAVLHCHQGVVHRDLKPENLLASKCKGAAYKLADFGLAIEVGQDQAWFGAGTGGY 180  
 DB 121 LEAVLHCHQGVVHRDLKPENLLASKCKGAAYKLADFGLAIEVGQDQAWFGAGTGGY 180  
 QY 181 LSPEVLKREAYGKPDVWACGVILYLLVGYPPFWDEDQHKLYQQIKAGAYDFPSPWD 240  
 DB 181 LSPEVLKREAYGKPDVWACGVILYLLVGYPPFWDEDQHKLYQQIKAGAYDFPSPWD 240  
 QY 241 YTPKAKNLINQMLTINPAKRTTAHEALKHPWCORSTVASMHRQETVECLKFNARRKL 300  
 DB 241 YTPKAKNLINQMLTINPAKRTTAHEALKHPWCORSTVASMHRQETVECLKFNARRKL 300  
 QY 301 KGAILTMTLRNFSVGRQTAPATMTSTAASGTMGLVQAKSLNKKADGVKPTQNSTK 360  
 DB 301 KGAILTMTLRNFSVGRQTAPATMTSTAASGTMGLVQAKSLNKKADGVKPTQNSTK 360  
 QY 361 NSAAATSPKGLPFAALEPQTTVIHNPVDGKSSDSANTTIEDAKARQEIKITTEQ 420  
 DB 361 NSAAATSPKGLPFAALEPQTTVIHNPVDGKSSDSANTTIEDAKARQEIKITTEQ 420  
 QY 421 LIEAVNNGDFEAYAFYFENLLAKNSKPITHTILNPHVHVGEDAAACIAYIRLTOYIDGQG 480  
 DB 421 LIEAVNNGDFEAYAFYFENLLAKNSKPITHTILNPHVHVGEDAAACIAYIRLTOYIDGQG 480  
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 DB 481 RPRTSQSEETRVVHRDQKQWVHFCSGAPVAPLQ 516  
 RESULT 2  
 ABP70158  
 ID ABP70158 standard; Protein; 542 AA.  
 XX  
 AC ABP70158;  
 XX  
 DT 07-APR-2003 (first entry)  
 XX  
 DE Amino acid sequence of oestrogen receptor alpha cofactor CF19.  
 XX  
 KW Human; oestrogen receptor alpha; ER-alpha; CF16; CF17; CF18; CF19; CF40;  
 KW CF41; CF42; CF43; cofactor; osteoporosis; bone disease; reproduction;  
 KW hormonal dysfunction; cancer; cardiovascular disease; atherosclerosis;  
 KW hot flush; mood change; Alzheimer's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200270699-A2.

XX PD 12-SEP-2002.

XX PF 28-FEB-2002; 2002WO-EP02189.

XX PR 01-MAR-2001; 2001EP-0105062.

XX PA (LION-) LION BIOSCIENCE AG.

XX PI Albers M, Ellwanger S, Loesser E, Koegl M;

XX DR WPI; 2002-713451/77.

XX DR N-PSDB; AB223378.

XX PT New cofactors of estrogen receptor alpha, designated as CF16, CF17, CF18, CF19, CF40, CF41, CF42 and/or CF43, useful for screening of compounds for treating osteoporosis, hormonal dysfunctions, cancer or cardiovascular diseases -

XX PS Claim 12; Page 76-78; 111pp; English.

XX CC The present sequence represents a cofactor of oestrogen receptor alpha (ER-alpha), designated CF19. The specification describes CF16, CF17, CF18, CF19, CF40, CF41, CF42, and CF43. The cofactor polypeptides and nucleic acid molecules are useful for screening for compounds for treating osteoporosis and other bone diseases, failures in reproductive functions or hormonal dysfunctions, cancer or cardiovascular diseases such as atherosclerosis, and in preventing hot flushes, mood changes and Alzheimer's disease. The CF proteins are also useful for screening for ligands of the ER alpha. The nucleic acid sequences are useful for making vectors and CF polypeptides, transforming host cells, as research tools for developing nucleic acid probes, and for developing analytical tools such as antisense oligonucleotides.

SQ Sequence 542 AA;

Query Match 99.2%; Score 2692; DB 23; Length 542;  
 Best Local Similarity 95.2%; Pred. No. 2e-249;  
 Matches 516; Conservative 0; Mismatches 0; Indels 26; Gaps 1;

QY 1 MATTVCFRFDEYQVLEDEIGKAFSVVRVCVKLCTGHEYAAKIINTKLSARDHOKLER 60  
 DB 1 MATTVCFRFDEYQVLEDEIGKAFSVVRVCVKLCTGHEYAAKIINTKLSARDHOKLER 60

QY 61 EARICLLKHSNIVRLHDSISESGPHYLVDLVITGGELFEDIVAREYVSEADASHCIQOI 120  
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QY 121 LEAVLCHQMGVVRHDLKPNELLASKCKGAAGVLADEGLAIEVQGDQOAWFGAGTGGY 180  
 DB 121 LEAVLCHQMGVVRHDLKPNELLASKCKGAAGVLADEGLAIEVQGDQOAWFGAGTGGY 180

QY 181 LSEVLRKEAYGKVPDIWAGVILYLLVGYPPFWEDEQKLYQKAGAYDFSPWDIT 240  
 DB 181 LSEVLRKEAYGKVPDIWAGVILYLLVGYPPFWEDEQKLYQKAGAYDFSPWDIT 240

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 DB 361 NSAAATSPKGTLPAALEPQTIVHNPVDGKESDSANTTIEDAKARKOEILKTTEQ 420

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DB 481 PHVHVGEDAACTAIYIRLTQYIDGGRPTSSQSEETRVWHRDQKQWVHFCSGAPVAP 540

QY 515 LQ 516  
 DB 541 LQ 542

RESULT 3  
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 ID AAY68791 standard; Protein; 641 AA.  
 XX AC AAY68791;  
 XX DT 16-MAY-2000 (first entry)  
 XX DE Amino acid sequence of a human phosphorylation effector PHSP-23.  
 XX KW Human; phosphorylation effector; PHSP; proliferative disorder;  
 XX KW immune disorder; neuronal disorder.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FH Domain 14..272  
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 XX 10-FEB-2000.  
 XX 28-JUL-1999; 99WO-US17132.  
 XX 28-JUL-1998; 98US-0123494.  
 PR 14-SEP-1998; 98US-0152814.  
 PR 14-OCT-1998; 98US-0173482.  
 PR 03-NOV-1998; 98US-0106889.  
 PR 19-NOV-1998; 98US-0109093.  
 PR 22-DEC-1998; 98US-0113796.  
 PR 12-JAN-1999; 99US-0173482.  
 PR 12-JAN-1999; 99US-0229005.  
 XX (INCY-) INCYTE PHARM INC.  
 XX Hillman JL, Lal P, Tang YT, Corley NC, Guegler KJ, Baughn MR;  
 PI Patterson C, Bandman O, Au-Young J, Gorgone GA, Yue H, Azimzai Y;  
 PI Reddy R, Lu DAM, Shih LL;  
 XX WPI: 2000-183125/16.  
 DR N-PSDB; AA246155.  
 XX  
 XX New human phosphorylation effectors useful for the diagnosis, treatment  
 PT and prevention of proliferative, immune and neuronal disorders -  
 XX  
 XX Claim 1; Page 101-103; 142pp; English.  
 XX  
 XX AAY68769-95 and AAY68797-99 represent human phosphorylation effectors  
 CC (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not  
 CC given in the specification). The sequences were isolated from cDNA  
 CC libraries prepared from various human tissues. The PHSP proteins are  
 CC useful for the diagnosis, treatment and prevention of proliferative  
 CC disorders, immune disorders and neuronal disorders. The PHSP proteins  
 CC form pharmaceutical compositions which useful for treating or preventing  
 CC disorders associated with decreased PHSP expression/activity. PHSP  
 CC antagonists are useful for treating or preventing disorders associated  
 CC with increased PHSP expression/activity.  
 XX  
 XX Sequence 503 AA;  
 SQ  
 Query Match 90.1%; Score 2445.5; DB 21; Length 503;  
 Best Local Similarity 87.6%; Pred. No. 9e-226;  
 Matches 475; Conservative 0; Mismatches 2; Indels 65; Gaps 3;  
 QY 1 MATTVTCTRTDEYQLYEDIGKGFVSVVRCVKLCGHEYAAKIINTKLSARDHQKLER 60  
 DB 1 MATTVTCTRTDEYQLYEDIGKGFVSVVRCVKLCGHEYAAKIINTKLSARDHQKLER 60

QY 61 EARICRLKHSNIVRLHDSISEGFGHYLVFDLVTGGEFEDIVAREYTSADASHCIIQOI 120  
 DB 61 EARICRLKHSNIVRLHDSISEGFGHYLVFDLVTGGEFEDIVAREYTSADASHCIIQOI 120  
 QY 121 LEAVLHCHOMGVVVRDLKPEKLLASCKGAAVKLADFGLAIEVQGGQAAWFGAGTPOY 180  
 DB 121 LEAVLHCHOMGVVVRDLKPEKLLASCKGAAVKLADFGLAIEVQGGQAAWFGAGTPOY 180  
 QY 181 LSPVLRKEAYGKPYDIWACGVILYILLVGYPPFWDQHKLYQOIKAGAYDFPSPEDWT 240  
 DB 181 LSPVLRKEAYGKPYDIWACGVILYILLVGYPPFWDQHKLYQOIKAGAYDFPSPEDWT 240  
 QY 241 VTPEAKNLINOMLTINPAKRITAEALKHPWVQCORSTVASMHRQETVECLIKKFNARRKL 300  
 DB 241 VTPEAKNLINOMLTINPAKRITAEALKHPWVQCORSTVASMHRQETVECLIKKFNARRKL 300  
 QY 301 KGAILTTMLATRNFSVGRQTTAPATMTAAAGTTMGLVQAKSLINKKADGVKPTQNSYK 360  
 DB 301 KGAILTTMLATRNFS- - - - -AKSLINKKADGVKPTQNSYK 360  
 QY 361 NSAAATSPKGTLPAPALPEQTTVIHNPVDGIKESSDASANTTIEDAKAKQSHIITTKTQ 420  
 DB 361 NSAAATSPKGTLPAPALPEQTTVIHNPVDGIKESSDASANTTIEDAKAKQSHIITTKTQ 420  
 QY 421 LIEAVNNGDFEAYAKICDPGLTSPFEPALNVLVEGMDPHRFENLLAKSKPHTHTILN 441  
 DB 421 LIEAVNNGDFEAYAKICDPGLTSPFEPALNVLVEGMDPHRFENLLAKSKPHTHTILN 441  
 QY 455 PHVHIGEDAAACIAXIRLTQYIDQGRPTSQSEETRVVHRRDGKQNVHFGSGAPVAP 514  
 DB 455 PHVHIGEDAAACIAXIRLTQYIDQGRPTSQSEETRVVHRRDGKQNVHFGSGAPVAP 514  
 QY 515 LQ 516  
 DB 502 LQ 503  
 RESULT 5  
 AAE16276  
 ID AAE16276 standard; Protein; 588 AA.  
 XX  
 AC AAE16276;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Human kinase PKIN-22 protein.  
 XX  
 KW Human; kinase; PKIN-22; cancer; leukaemia; adenocarcinoma; osteoporosis;  
 KW Immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;  
 KW Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;  
 KW allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;  
 KW autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis;  
 KW Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;  
 KW rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;  
 KW hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;  
 KW cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;  
 KW congestive heart failure; ischaemic heart disease; lung tumour; gout;  
 KW fatty liver; Niemann-Pick's disease; gene therapy; chromosome 10.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT 14..272  
 FT Domain /note= "Eukaryotic protein kinase domain"  
 FT 15..263  
 FT Domain /label= Protein\_kinase\_domain  
 FT 18..263 /label= Protein\_kinase\_domain  
 FT 20..262 /label= Protein\_kinase\_domain  
 XX  
 PN WO200196547-A2.

XX 20-DEC-2001.  
 XX 14-JUN-2001; 2001WO-US19444.  
 XX 15-JUN-2000; 2000US-212073P.  
 XX 23-JUN-2000; 2000US-213467P.  
 XX 30-JUN-2000; 2000US-215651P.  
 XX 07-JUL-2000; 2000US-216605P.  
 XX 13-JUL-2000; 2000US-218372P.  
 XX 25-AUG-2000; 2000US-228056P.  
 XX (INCY-) INCYTE GENOMICS INC.  
 XX Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y;  
 PI Gandhi AR, Tribouley CA, Wallia NK, Yao MG, Lu DAM, Greenwald SR;  
 PI Ramkumar JR, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT;  
 PI Baughn MR, He A, Thorton M, Hafalia A, Patterson C, Gururajan R;  
 PI Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L;  
 PI Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;  
 XX WPI; 2002-090207/12.  
 DR N-PSDB; RAD26469.  
 XX New polypeptides, useful for diagnosing, treating or preventing  
 PT disorders of growth and development, cardiovascular and lipid, and  
 PT diseases such as cancer, comprise human kinase polypeptides -  
 XX Claim 1; Page 167-168; 197pp; English.  
 XX The invention relates to human kinase PKIN proteins and their  
 CC corresponding cDNAs. A composition containing PKIN agonist is useful for  
 CC treating a disease or condition associated with decreased expression of  
 CC PKIN and a composition comprising PKIN antagonist is useful for treating  
 CC a disease or condition associated with overexpression of PKIN. The  
 CC disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,  
 CC myeloma, sarcoma, teratocarcinoma, Hodgkin's disease), immune disorder  
 CC (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,  
 CC atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,  
 CC autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes  
 CC mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,  
 CC osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,  
 CC rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,  
 CC bacterial, parasitic, fungal, viral, protozoal and helminthic infections)  
 CC growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,  
 CC Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio  
 CC vascular disease (arteriovenous fistula, hypertension, myocarditis,  
 CC aneurysms, congestive heart failure, angina pectoris, vasculitis,  
 CC ischaemic heart disease, chronic bronchitis, lung tumours); lipid  
 CC disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,  
 CC hypcholesterolaemia, obesity). PKIN DNA is useful for assessing  
 CC toxicity of a test compound and in gene therapy. The present sequence  
 CC is human PKIN-22 protein. Human PKIN-22 gene is located on  
 CC chromosome 10.  
 XX Sequence 588 AA;  
 Query Match 82.5%; Score 2241; DB 23; Length 588;  
 Best Local Similarity 73.8%; Fred. No. 5.4e-206;  
 Matches 437; Conservative 34; Mismatches 41; Indels 80; Gaps 5;  
 Qy 1 MATTVTCTRETDYQLYEDIGKGFASVVRVRCVKLTGFEYAAKIINTKLSARDHOKLER 60  
 Db 1 MATTATCTRTDDYQLFEEELGKGFASVVRVRCVKLTSTQYAAKIINTKLSARDHOKLER 60  
 Qy 61 EARCRLKSNIVRLHDSISEGPHYLVDLVTGELFEDIVAREYSEADASHCICQI 120  
 Db 61 EARCRLKHPNIVRLHDSISEGPHYLVDLVTGELFEDIVAREYSEADASHCICQI 120  
 Qy 121 LEAVLHCHQGVVHRLKPEINLLASKCKGAAYKADFGIALEVGGDQAAWFGAGTFCY 180  
 Db 121 LESVNHVHQHDIHRLKPEINLLASKCKGAAYKADFGIALEVGGDQAAWFGAGTFCY 180

Qy 181 LSPEVLREAYKPVDIWACGVILYLLVGYPPFWEDQHKLYQQIKAGAYDPSPWDOT 240  
 Db 181 LSPEVLREAYKPVDIWACGVILYLLVGYPPFWEDQHKLYQQIKAGAYDPSPWDOT 240  
 Qy 241 VYPEAKNLINOMLTINPAKRITAEALHPWVQORSTVASMMHROPTVECLKFNARKKL 300  
 Db 241 VYPEAKNLINOMLTINPAKRITADQRLKIPWQORSTVASMMHROPTVECLKFNARKKL 300  
 Qy 301 KGAILTMTLATRNPSYGRQTTAPATMTASTAGTTMGLVQAKSLNKKADG----- 351  
 Db 301 KGAILTMTLSRNFVSQROSSAPASAAAGLA--GQAASLLNKKSDGGVKKRKS 357  
 Qy 352 ---VKPOFNSTKNSAATSPKGTLPALRPQTTHNPVDGKIKESSDSANTTDEEDAK 408  
 Db 358 SYHLMFQSN--KNSLVSPAQEPAPLOTAMEPQTTHNPVDGKIKESSDSANTTDEEDAK 416  
 Qy 409 A-----PKOEIKTTEQLEAVNNGDF 430  
 Db 417 AAPLRTGNGSSVPEGRSSRDRTAPASAGMQPQSLCSAMRKOEIKITEQLEAVNNGDF 476  
 Qy 431 EAYA-----FYFENLLAKNSKPIHTTILNPHVHVGEDA 464  
 Db 477 EAYTKIDPGLTSPPEALGNLVEGMDPHKFFENLLSKNSKPIHTTILNPHVHVGEDA 536  
 Qy 465 ACIAYIRLTQYIDGGPRPTSQSEETRYVHRRDGKQWNVHFCGSGAPVAPLQ 516  
 Db 537 ACIAYIRLTQYIDGGPRPTSQSEETRYVHRRDGKQWNVHFCGSGAPVAPLQ 588  
 RESULT 6  
 AAM79441  
 ID AAM79441 standard; Protein; 525 AA.  
 XX AC AAM79441;  
 XX DT 06-NOV-2001 (first entry)  
 XX DE Human protein SEQ ID NO 3087.  
 XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 XX KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 XX KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 XX KW nervous system disorder; arthritis; inflammation.  
 XX OS Homo sapiens.  
 XX WO200157190-A2.  
 XX PD 09-AUG-2001.  
 XX PF 05-FEB-2001; 2001WO-US04098.  
 XX PR 03-FEB-2000; 2000US-0496914.  
 XX PR 27-APR-2000; 2000US-0560875.  
 XX PR 20-JUN-2000; 2000US-0598075.  
 XX PR 19-JUL-2000; 2000US-0620325.  
 XX PR 01-SEP-2000; 2000US-0654936.  
 XX PR 15-SEP-2000; 2000US-0663561.  
 XX PR 20-OCT-2000; 2000US-0693325.  
 XX PR 30-NOV-2000; 2000US-0728422.  
 XX (HYSE-) HYSEQ INC.  
 XX PA Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;  
 XX PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
 XX PI Xue AU, Yang Y, Wejhrman T, Goodrich R;  
 XX WPI; 2001-476283/51.  
 XX DR N-PSDB; AAK52574.  
 XX Nucleic acids encoding polypeptides with cytokine-like activities,  
 PT useful in diagnosis and gene therapy -  
 XX



QY	61	EARICLLKHSNIVKLDHSISERGFHYLVDFDLVTGGELFEDIVAREYISEADASHCIQOI	120	FT	Modified-site	79..82	/note= "Casein kinase II phosphorylation site"
Db	68	EARICLLKHPNIVRLHDSISERGFHYLVDFDLVTGGELFEDIVAREYISEADASHCIHQI	127	FT	Modified-site	94..97	/note= "Casein kinase II phosphorylation site"
QY	121	LEAVLACHQGVVHDLKPEMLLASKCKRAVKLADGLAIEVQGDQAGFAGTGY	180	FT	Modified-site	109..112	/note= "Casein kinase II phosphorylation site"
Db	128	LESVNIHQHDIHVDLKPENLLASKCKRAVKLADGLAIEVQGDQAGFAGTGY	187	FT	Active-site	132..144	/note= "Serine/Threonine protein kinase active-site signature"
QY	181	LSPEVLKRAYGKPDIVACGVILYILVGYPPFDEQHKLYQOIKAGAYDFPSPWD	240	FT	Region	195..215	/label= Helix_1
Db	188	LSPEVLKDPYKGPVDIVACGVILYILVGYPPFDEQHKLYQOIKAGAYDFPSPWD	247	FT	Modified-site	259..262	/note= "CAMP- and cGMP-dependent protein kinase phosphorylation site"
QY	241	VTEAKNLIQMLTINPAKRITAEALKHPWCQSTVASMMHQEVECLRKFNARKL	300	FT	Modified-site	302..307	/note= "N-myristoylation site"
Db	248	VTEAKNLIQMLTINPAKRITADQALKHPWCQSTVASMMHQEVECLRKFNARKL	307	FT	Modified-site	313..316	/note= "Asn is N-glycosylated"
QY	301	KGAILTMTLAFNFSVGRQTTAPATMTAAAGTTMGLVEQAQSLNKKAD-GVYKPTNST	359	FT	Region	319..339	/label= Helix_2
Db	308	KGAILTMTLVSRNFA-----AKSLNKKSDGGVKPQSN--	342	FT	Modified-site	352..355	/note= "CAMP- and cGMP-dependent protein kinase phosphorylation site"
QY	360	KNSAATSPKGLPPALPOTTVIHPVDGKESDSANTTIEDAKARQEIKITTE	419	FT	Modified-site	353..356	/note= "CAMP- and cGMP-dependent protein kinase phosphorylation site"
Db	343	KNSLVPAQEPAPLQATMEPQTIVVHNATDGKIGKTESCNTTDEDLKYRQEIKITTE	402	FT	Modified-site	371..374	/note= "Asn is N-glycosylated"
QY	420	QLTEAVNNGDFEAY-----FYENLLAKNSKPIHTTIL	453	FT	Modified-site	375..380	/note= "N-myristoylation site"
Db	403	QLTEALNNGDFEAYTKICDPLGTSFPEALGNLVGMDFKFYENLLSKNSKPIHTTIL	462	FT	Modified-site	378..383	/note= "N-myristoylation site"
QY	454	NPHVHVIGDAACIAYIRLQYIDGQGRPTQSSETRVHRRDQKQNVHFCSGAPVA	513	FT	Modified-site	384..387	/note= "Asn is N-glycosylated"
Db	463	NPHVHVIGDAACIAYIRLQYIDGQGRPTQSSETRVHRRDQKQNVHFCSGAPAA	522	FT	Modified-site	385..388	/note= "Casein kinase II phosphorylation site"
QY	514	PLQ 516		FT	Modified-site	386..389	/note= "Casein kinase II phosphorylation site"
Db	523	PLQ 525		FT	Modified-site	387..390	/note= "Casein kinase II phosphorylation site"
RESULT 8				FT	Modified-site	400..405	/note= "Casein kinase II phosphorylation site"
AAE24635				FT	Modified-site	401..404	/note= "N-myristoylation site"
XX	AAE24635			FT	Modified-site	404..407	/note= "Asn is N-glycosylated"
XX	AAE24635			FT	Modified-site	405..433	/note= "Casein kinase II phosphorylation site"
22-OCT-2002 (first entry)				FT	Domain		/note= "Binding-protein dependent transport system inner membrane signature"
Human calcium/calmodulin-dependent protein kinase.				FT	Modified-site	410..412	/note= "Protein kinase C phosphorylation site"
Human; calcium/calmodulin-dependent protein kinase; enzyme; inflammation; Breast cancer; skin melanotic melanoma; adenocarcinoma; arteriosclerosis; Burkitt's lymphoma; uterus leiomyosarcoma; foetal brain tumour; vaccine; psoriasis; gene therapy; protein therapy; cytostatic; antiinflammatory; antiarteriosclerotic; chromosome 10.				FT	Modified-site	410..413	/note= "Casein kinase II phosphorylation site"
Homo sapiens.				FT	Modified-site	465..468	/note= "Casein kinase II phosphorylation site"
Key				FT	Modified-site	534..537	/note= "Casein kinase II phosphorylation site"
Binding-site	20..43	Location/Qualifiers		FT	Modified-site		/note= "Casein kinase II phosphorylation site"
FT	/note= "Protein kinase Atp-binding region signature domain"			XX			
FT	33..36			XX			
FT	/note= "CAMP- and cGMP-dependent protein kinase phosphorylation site"			XX			
FT	36..39			XX			
FT	/note= "Casein kinase II phosphorylation site"			XX			
FT	47..49			XX			
FT	/note= "Protein kinase C phosphorylation site"			XX			
FT	48..51			XX			
FT	/note= "CAMP- and cGMP-dependent protein kinase phosphorylation site"			XX			
FT	51..53			XX			
FT	/note= "Protein kinase C phosphorylation site"			XX			
FT	51..54			XX			
FT	/note= "Casein kinase II phosphorylation site"			XX			
US6387677-B1.				XX			
14-MAY-2002.				XX			
08-MAR-2001; 2001US-0800960.				XX			
08-MAR-2001; 2001US-0800960.				XX			
(PEKE ) PE CORP NY.				XX			
Ye J, Yan C, Di Francesco V, Beasley EM;				XX			
WPI; 2002-478444/51.				XX			
N-PSDB; AAD39316, AAD39317.				XX			



PT Nucleic acid molecules encoding calcium/calmodulin-dependent protein  
PT kinases, useful for preventing diagnosing and treating e.g. cancers,  
XX psoriasis and inflammation -  
XX  
PS Claim 1; Fig 2A; 85pp; English.  
XX  
CC The present invention relates to calcium/calmodulin-dependent protein  
CC kinases and polynucleotides encoding such proteins. Sequences of the  
CC invention are used as models for the development of human therapeutic  
CC targets, aid in the identification of therapeutic proteins and serve  
CC as targets for the development of human therapeutic agents that modulate  
CC kinase activity in cells and tissues that express the kinase. They are  
CC expressed in humans in the placenta, skin melanotic melanomas, breast  
CC cancers (including mammary adenocarcinoma), duodenal adenocarcinomas  
CC (small intestine), ovary adenocarcinomas, Burkitt's lymphomas (lymph),  
CC uterus leiomyosarcomas, foetal brain tumours and in disease conditions  
CC including inflammation, arteriosclerosis and psoriasis. Sequences of  
CC the invention are used in gene therapy and protein therapy. They are  
CC also used as vaccines. The present sequence is human calcium/calmodulin-  
CC dependent protein kinase. Calcium/calmodulin-dependent protein kinase  
CC genomic DNA is located on chromosome 10.  
XX  
SQ Sequence 565 AA;  
  
Query Match 82.0%; Score 2225.5; DB 23; Length 565;  
Best Local Similarity 74.7%; Pred. No. 1.6e-204;  
Matches 434; Conservative 30; Mismatches 36; Indels 81; Gaps 5;  
  
QY 1 MATTTCCTFFDYEDYIGKAFSVVRCVKLTGCHYAAKIINTKLSARDHOKLER 60  
DB 1 MATTATCTTDDYQYFEELGKAFSVVRCVKLTGCHYAAKIINTKLSARDHOKLER 60  
QY 61 EARTCLKNSVIRLHDSISEGPHYLVDLTGGLFEDIVAREYVSEADASHCICQI 120  
DB 61 EARTCLKNSVIRLHDSISEGPHYLVDLTGGLFEDIVAREYVSEADASHCICQI 120  
QY 121 LEAVLHCHQMGVHROLKPNILLASKCKGAANKLADFLGATEVQDQOAWFGFAGPPGY 180  
DB 121 LSVNHIHQHIDVHROLKPNILLASKCKGAANKLADFLGATEVQDQOAWFGFAGPPGY 180  
QY 181 LSPVLRKEAYGKPDVWACGVLYLLVGYPPFWDHOKLYQKIKAGAYDFSPBMDT 240  
DB 181 LSPVLRKDPYKPDVWACGVLYLLVGYPPFWDHOKLYQKIKAGAYDFSPBMDT 240  
QY 241 VPPEAKNLINQMLTINPAKRITAEALHPWVCORSTVASMHRQETVECLKKNARRKL 300  
DB 241 VPPEAKNLINQMLTINPAKRITADQALHPWVCORSTVASMHRQETVECLKKNARRKL 300  
QY 301 KGAILTTMLATNFSGVROQTAPATWSTAAGTTMGLVEQAKSLINKKAD-GVTPQNST 359  
DB 301 KGAILTTMLVSRNFSVGRQSSAPASPAASAAGLA---GQAASKSLNKKSDGVKKRKS 357  
QY 360 KNSAATSPKTLPPAALPQPTVTHNPVDGKSSDANTTLEDDAKA----- 409  
DB 358 S-----VHLMPEQTVVHNATDGKSTESCNTTDEDLKAPLRTNGSS 404  
QY 410 -----RKQELIKTTEQLIEAVNNGDFEAYA----- 434  
DB 405 VPEGRSRDRTPASAGMQPOPILCSSAMRKQELIKTTEQLIEAVNNGDFEAYTRICDPGL 464  
QY 435 -----FYPENLLAKNSKPIHTTILNPHVHVGEDAACIAVIRLTOY 475  
DB 465 TTFEPALGNLVGMDPHKPYFENLLSKNSKPIHTTILNPHVHVGEDAACIAVIRLTOY 524  
QY 476 IDGQGRPTSQSEETRWHRDCKWONVHFHCSGAPVAPLQ 516  
DB 525 IDGQGRPTSQSEETRWHRDCKWONVHFHCSGAPVAPLQ 565  
  
RESULT 9  
ABG75873  
ID ABG75873 standard; Protein; 565 AA.  
XX

AC ABG75873;  
XX 02-MAY-2003 (first entry)  
XX  
XX DE Novel human kinase.  
XX  
XX Human; calcium/calmodulin-dependent protein kinase subfamily;  
KW kinase; cancer; inflammation; arteriosclerosis; psoriasis;  
KW mammary adenocarcinoma; skin melanotic melanoma; ovary adenocarcinoma;  
KW uterus leiomyosarcoma; Burkitt's lymphoma; duodenal adenocarcinoma;  
KW enzyme.  
XX  
XX Homo sapiens.  
OS  
XX Key Location/Qualifiers  
XX Regio 20..43  
XX /note= "Protein kinases ATP-binding region signature"  
XX Modified-site 33..36  
XX /note= "CAMP- and CGMP-dependent protein kinase  
XX phosphorylation site"  
XX Modified-site 36..39  
XX /note= "Casein kinase II phosphorylation site"  
XX Modified-site 47..49  
XX /note= "Protein kinase C phosphorylation site"  
XX Modified-site 48..51  
XX /note= "CAMP- and CGMP-dependent protein kinase  
XX phosphorylation site"  
XX Modified-site 51..53  
XX /note= "Protein kinase C phosphorylation site"  
XX Modified-site 51..54  
XX /note= "Casein kinase II phosphorylation site"  
XX Modified-site 79..82  
XX /note= "Casein kinase II phosphorylation site"  
XX Modified-site 94..97  
XX /note= "Casein kinase II phosphorylation site"  
XX Modified-site 109..112  
XX /note= "Casein kinase II phosphorylation site"  
XX Region 132..144  
XX /note= "Serine/Threonine protein kinases active-site  
XX signature"  
XX Modified-site 259..262  
XX /note= "CAMP- and CGMP-dependent protein kinase  
XX phosphorylation site"  
XX Modified-site 302..307  
XX /label= N-myristoylation\_site  
XX Modified-site 313..316  
XX /label= N-glycosylation\_site  
XX Modified-site 352..355  
XX /note= "CAMP- and CGMP-dependent protein kinase  
XX phosphorylation site"  
XX Modified-site 353..356  
XX /note= "CAMP- and CGMP-dependent protein kinase  
XX phosphorylation site"  
XX Modified-site 371..374  
XX /label= N-glycosylation\_site  
XX Modified-site 375..380  
XX /label= N-myristoylation\_site  
XX Modified-site 378..383  
XX /label= N-myristoylation\_site  
XX Modified-site 384..387  
XX /label= N-glycosylation\_site  
XX Modified-site 385..388  
XX /note= "Casein kinase II phosphorylation site"  
XX Modified-site 386..389  
XX /note= "Casein kinase II phosphorylation site"  
XX Modified-site 387..390  
XX /note= "Casein kinase II phosphorylation site"  
XX Modified-site 400..405  
XX /label= N-myristoylation\_site  
XX Modified-site 401..404  
XX /label= N-glycosylation\_site  
XX Modified-site 404..407  
XX /note= "Casein kinase II phosphorylation site"



XX The invention relates to polynucleotides (AAK51456-AAK53435) and the  
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation.  
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666  
 CC (AAM80020) are omitted as the relevant pages from the sequence listing  
 CC were missing at the time of publication.  
 XX  
 SQ Sequence 518 AA;  
 Query Match 81.8%; Score 2222; DB 22; Length 518;  
 Best Local Similarity 79.0%; Pred. No. 2.9e-204;  
 Matches 429; Conservative 25; Mismatches 37; Indels 52; Gaps 4;  
 QY 1 MATVTCTRTDEYQLYEDIGKGFVSVVRCVKLCTGHEYAAKIINTKKLSARDHOKLER 60  
 DB 1 MATATCTRTDDYQLFELGKGFVSVVRSVKKTSTHEYAAKIINTKKLSARDHOKLER 60  
 QY 61 EARICLLKHSNIVRLHDSISEGPHYLVDLTGTGELFIVAREYVSEADASHCICQI 120  
 DB 61 EARICLLKHPNIVRLHDSISEGPHYLVDLTGTGELFIVAREYVSEADASHCICQI 120  
 QY 121 LEAVLHCHQVGVHRLDKPENLLASKCKGAAYKVLADFGLAIEVQDQQAQWFGAGTGGY 180  
 DB 121 LESVNHCHQVGVHRLDKPENLLASKCKGAAYKVLADFGLAIEVQDQQAQWFGAGTGGY 180  
 QY 181 LSPVLRKEAYGKPVDIWACGVILYLLVGYPPFWEDQHKLYQKIKAGADTFSPSPWT 240  
 DB 181 LSPVLRKEAYGKPVDIWACGVILYLLVGYPPFWEDQHKLYQKIKAGADTFSPSPWT 240  
 QY 241 VTPKAKLINQMLTINPAKRITAEALKHPWCQVSTVSMHROETVECLKFNARRKL 300  
 DB 241 VTPKAKLINQMLTINPAKRITAEALKHPWCQVSTVSMHROETVECLKFNARRKL 300  
 QY 301 KGAITMTLAFNSVGRGTTAPATMSTASGTTMGLVBOAKSLNKKAD-GVKPQNST 359  
 DB 301 KGAITMTLAFNSVGRGTTAPATMSTASGTTMGLVBOAKSLNKKAD-GVKPQNST 359  
 QY 360 KNSAATSPKGTLPALPQPTVTHNPVQGIKESDSANTTIEDAKARKQELIKTE 419  
 DB 360 KNSAATSPKGTLPALPQPTVTHNPVQGIKESDSANTTIEDAKARKQELIKTE 419  
 QY 420 QLIEAVNNGDFEAYA-----FYFENLLAKNSKPIHTTIL 453  
 DB 420 QLIEAVNNGDFEAYA-----FYFENLLAKNSKPIHTTIL 453  
 QY 454 NPHVHVGEDAACIAVIRLTQYIDQGRPTQSSEETRVWHRDQKQWVPHGSGAPVA 513  
 DB 454 NPHVHVGEDAACIAVIRLTQYIDQGRPTQSSEETRVWHRDQKQWVPHGSGAPVA 513  
 QY 514 PLQ 516  
 DB 516 PLQ 518  
 RESULT 11  
 ID AAK03512 standard; Protein; 499 AA.  
 AC AAK03512;  
 DT 12-SEP-2001 (first entry)  
 DE Human protein kinase #12.  
 XX

KW Human; protein kinase; PTK; STK; cancer; cardiovascular disease;  
 KW metabolic disorder; immune related disease; neurological disorder;  
 KW neurodegenerative disorder; inflammatory disorder; infectious disease;  
 XX reproductve disorder.  
 OS Homo sapiens.  
 XX WO200138503-A2.  
 XX 31-MAY-2001.  
 XX 22-NOV-2000; 2000WO-US32085.  
 XX 24-NOV-1999; 99US-0167482.  
 XX (SUG- ) SUGEN INC.  
 XX Ploymann GD, Whyte D, Manning G, Sudarsanam S, Martinez R;  
 XX Flanagan P, Clary D;  
 XX WPI; 2001-343950/36.  
 XX N-PSDB; AAS06712.  
 XX Nucleic acids encoding human kinase polypeptides, useful for preventing  
 XX diagnosing and/or treating e.g. cancer, immune, cardiovascular and  
 XX neuronal-associated diseases, and microbial infections -  
 XX Claim 7; Figure 2; 433pp; English.  
 XX AAU03501-AAU03557 represent novel human protein kinases #1-57. The  
 CC novel protein kinases have been identified as members of the tyrosine  
 CC or serine/threonine kinase (PTK and STK) families. The polynucleotides  
 CC encoding protein kinases and the polypeptides may be used in the  
 CC prevention, diagnosis and treatment of diseases associated with  
 CC inappropriate kinase expression. For example, they may be used to treat  
 CC cancers (especially cancers of haematopoietic origin), cardiovascular  
 CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),  
 CC immune related diseases (e.g. rheumatoid arthritis), neurological  
 CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.  
 CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious  
 CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).  
 CC Additionally, polynucleotides encoding protein kinases may be  
 CC used for gene therapy and as DNA probes in diagnostic assays.  
 CC The protein kinase polypeptides may be used as antigens in the production  
 CC of antibodies against the protein kinases and in assays to identify  
 CC modulators of protein kinase expression and activity.  
 XX  
 SQ Sequence 499 AA;  
 Query Match 76.2%; Score 2070; DB 22; Length 499;  
 Best Local Similarity 73.1%; Pred. No. 1.1e-189;  
 Matches 396; Conservative 31; Mismatches 25; Indels 90; Gaps 3;  
 QY 1 MATVTCTRTDEYQLYEDIGKGFVSVVRCVKLCTGHEYAAKIINTKKLSARDHOKLER 60  
 DB 1 MATVTCTRTDEYQLYEDIGKGFVSVVRCVKLCTGHEYAAKIINTKKLSARDHOKLER 60  
 QY 61 EARICLLKHSNIVRLHDSISEGPHYLVDLTGTGELFIVAREYVSEADASHCICQI 120  
 DB 61 EARICLLKHPNIVRLHDSISEGPHYLVDLTGTGELFIVAREYVSEADASHCICQI 120  
 QY 121 LEAVLHCHQVGVHRLDKPENLLASKCKGAAYKVLADFGLAIEVQDQQAQWFGAGTGGY 180  
 DB 121 LESVNHCHQVGVHRLDKPENLLASKCKGAAYKVLADFGLAIEVQDQQAQWFGAGTGGY 180  
 QY 181 LSPVLRKEAYGKPVDIWACGVILYLLVGYPPFWEDQHKLYQKIKAGADTFSPSPWT 240  
 DB 181 LSPVLRKEAYGKPVDIWACGVILYLLVGYPPFWEDQHKLYQKIKAGADTFSPSPWT 240  
 QY 241 VTPKAKLINQMLTINPAKRITAEALKHPWCQVSTVSMHROETVECLKFNARRKL 300  
 DB 241 VTPKAKLINQMLTINPAKRITAEALKHPWCQVSTVSMHROETVECLKFNARRKL 300



DB 417 PHVHLGDDAACIAYIRLTQMDGSGPKTMOSEETRYVHRRDQKQWVHFRSGSPVP 476  
 QY 515 LQ 516  
 DB 477 IK 478

1 MATTVTCTRTDEYQYVEDIGKAFSVVRKCVKCTGHEYAAKIINTKLSARDHQKLER 60  
 107 MASTTCTRTDEYQYVEELGKAFSVVRKCVKCTGHEYAAKIINTKLSARDHQKLER 166  
 61 EARICRLKHSNIVRLHDSISEGPHYLVDLYVGGELFEDIVAREYYSADASHCIQOI 120  
 167 EARICRLKHSNIVRLHDSISEGPHYLVDLYVGGELFEDIVAREYYSADASHCIQOI 226  
 121 LEAVLHCHOMGVHRLDLKPNLILASKKGAAYKADFLAIEVQDQQAQWFGAGTGGY 180  
 227 LSVNHECHLNGIVHRLDLKPNLILASKKGAAYKADFLAIEVQDQQAQWFGAGTGGY 286  
 181 LSPVLRKAYKQVDIWAQGVILYILVGYPPFWDEQHLKYOQIKAGYDFFSPENDT 240  
 287 LSPVLRKAYKQVDIWAQGVILYILVGYPPFWDEQHLKYOQIKAGYDFFSPENDT 346  
 241 VTPKAKLINOMLTINPAKRTAHEALKHPVVCORSTVSMHROETVCLKKNFARKKL 300  
 347 VTPKAKLINOMLTINPAKRTAHEALKHPVVCORSTVSMHROETVCLKKNFARKKL 406  
 301 KGAILTTMLATRNFSVGRQTTAPATMTAAAGTTMGLVQAKSLNKKADGVKQPTNSTK 360  
 407 KGAILTTMLATRNFSVGRQTTAPATMTAAAGTTMGLVQAKSLNKKADGVKQPTNSTK 430  
 361 NSAAATSPKGLTPPALEPQTTVHNPDVGIKESDSANTTIEDAKARKOEIIKTTEQ 420  
 431 NSAAATSPKGLTPPALEPQTTVHNPDVGIKESDSANTTIEDAKARKOEIIKTTEQ 462  
 421 LIEAVNNGDFEAYKICDPCGTAPEALGNLVEGMOFHRFYFENALSKNPKIHTILN 454  
 463 LIEAVNNGDFEAYKICDPCGTAPEALGNLVEGMOFHRFYFENALSKNPKIHTILN 522  
 455 PHVHVGDDAACIAYIRLTQMDGSGPKTMOSEETRYVHRRDQKQWVHFRSGSPVP 514  
 523 PHVHVGDDAACIAYIRLTQMDGSGPKTMOSEETRYVHRRDQKQWVHFRSGSPVP 582  
 515 LQ 516  
 583 IK 584

RESULT 14  
 ABB65515  
 ID ABB65515 standard; Protein; 493 AA.  
 AC ABB65515;  
 XX  
 DT 26-MAR-2002 (first entry)  
 DE Drosophila melanogaster polypeptide SEQ ID NO 23337.  
 KW Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.  
 OS Drosophila melanogaster.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 XX  
 PF 23-MAR-2001; 2001WO-US09231.  
 XX  
 PR 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers BW;  
 DR WPI; 2001-656850/75.  
 DR N-PSDB; ABL09618.  
 XX

ABG16826  
 ID ABB65515 standard; Protein; 605 AA.  
 AC ABB65515;  
 XX  
 DT 13-FEB-2002 (first entry)  
 DE Novel human diagnostic protein #16817.  
 XX  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.  
 KW  
 OS Homo sapiens.  
 XX  
 PN WO200175067-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US08631.  
 XX  
 PR 31-MAR-2000; 2000US-0540217.  
 PR 23-AUG-2000; 2000US-0649167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 XX  
 DR WPI; 2001-639362/73.  
 DR N-PSDB; AAS81013.  
 XX  
 XX New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -  
 PS Claim 20; SEQ ID NO 47185; 103pp; English.  
 XX  
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 XX Sequence 605 AA;  
 Query Match 76.1%; Score 2067; DB 22; Length 605;  
 Best Local Similarity 72.3%; Pred. No. 3e-189;  
 Matches 395; Conservative 32; Mismatches 25; Indels 90; Gaps 3;

PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX  
 XX  
 PS Disclosure; SEQ ID NO 23337; 21pp + Sequence Listing; English.  
 XX  
 XX The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins  
 CC (ABB57737-ABB72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 XX Sequence 493 AA;

Query Match 69.0%; Score 1872; DB 22; Length 493;  
 Best Local Similarity 67.0%; Pred. No. 1.2e-170;  
 Matches 361; Conservative 42; Mismatches 46; Indels 90; Gaps 5;  
 QY 1 MATVTCRTFDEVQYLEDIGKGFVSVRCVKLTGHEYAAKIINTKLSARDHQKLER 60  
 Db 1 MAAPAACTRFSDNYDIKEELGKGFVSVRCVKLTGHEYAAKIINTKLTARDFOKLER 60  
 QY 61 EARICRLKHSNIVRLHDSISEGPHYLVFLDTGGLFEDIVAREYSEADASHCICQI 120  
 Db 61 EARICRLKHSNIVRLHDSIQENYHYLVFLDTGGLFEDIVAREYSEADASHCICQI 120  
 QY 121 LEAVLHCHQGVVHRDLKPENLLASKCKGAALKADFLGLAIEVQGDQAWFGFAGTGY 180  
 Db 121 LESVNHCHQGVVHRDLKPENLLASKCKGAALKADFLGLAIEVQGDQAWFGFAGTGY 180  
 QY 181 LSPVLRKEAGKPVDMWAGVILYLLVGPFWDEDOHKLQIKAGAYDPPSPWDT 240  
 Db 181 LSPVLRKEAGKPVDMWAGVILYLLVGPFWDEDOHKLQIKAGAYDPPSPWDT 240  
 QY 241 VTPEAKNLINQMLTINPAKRITAEALKHPWCQRTSVASMMHROETVECLKFNARRKL 300  
 Db 241 VTPEAKNLINQMLTINPAKRITAEALKHPWCQRTSVASMMHROETVECLKFNARRKL 300  
 QY 301 KGAILTMTLATRNFS--VGRQTAPATMTAAAGTMTGLVQAKSLNKKADGVKPTQNS 358  
 Db 301 KGAILTMTLATRNFSKFTGR-----SMITKKGESQ----- 331  
 QY 359 TKNSAATSPKGTLPAPALEPQTVIHNVPDGIKSSDSANTTIEDDAK-ARKQETIKT 417  
 Db 332 -----VKSTDSSTILEDDEDDKARARQEIHKI 359  
 QY 418 TEQILAVNNGDFEAYA-----FYFENLAKNSKPIHTT 451  
 Db 360 TEQILAINSGDFDFTKICDPHLTAPEALGNLVEGIDPHKTFYFENLVGNKCAINT 419  
 QY 452 ILAPHVHVGEDACIAVRLTQYIDQGRPTTSOETRYVHRDCKWQNFHCSGA 510  
 Db 420 ILAPHVHLLGEAACTAIVRITQIDKQGHATHOSEETRVVHMKRONKQNVHFRSAS 478

## RESULT 15

AB066655  
 ID AB066655 standard; Protein; 493 AA.  
 XX  
 AC AB066655;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster polypeptide SEQ ID NO 26757.  
 XX  
 KW Drosophila; developmental biology; cell signalling; insecticide;  
 pharmaceutical.

XX Drosophila melanogaster.  
 OS WO200171042-A2.  
 XX  
 XX 27-SEP-2001.  
 PD  
 XX 23-MAR-2001; 2001WO-US09231.  
 PF  
 XX 23-MAR-2000; 2000US-191637P.  
 XX  
 PR 11-JUL-2000; 2000US-061415O.  
 PR  
 XX (PEKE ) PE CORP NY.  
 XX  
 XX Venter JC, Adams M, Li PWD, Myers EW;  
 FI WPI; 2001-656860/75.  
 DR N-PSDB; ABL10758.  
 DR  
 XX New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX  
 PS Disclosure; SEQ ID NO 26757; 21pp + Sequence Listing; English.  
 XX  
 XX The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins  
 CC (ABB57737-ABB72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 XX Sequence 493 AA;  
 SQ  
 Query Match 69.0%; Score 1872; DB 22; Length 493;  
 Best Local Similarity 67.0%; Pred. No. 1.2e-170;  
 Matches 361; Conservative 42; Mismatches 46; Indels 90; Gaps 5;  
 QY 1 MATVTCRTFDEVQYLEDIGKGFVSVRCVKLTGHEYAAKIINTKLSARDHQKLER 60  
 Db 1 MAAPAACTRFSDNYDIKEELGKGFVSVRCVKLTGHEYAAKIINTKLTARDFOKLER 60  
 QY 61 EARICRLKHSNIVRLHDSISEGPHYLVFLDTGGLFEDIVAREYSEADASHCICQI 120  
 Db 61 EARICRLKHSNIVRLHDSIQENYHYLVFLDTGGLFEDIVAREYSEADASHCICQI 120  
 QY 121 LEAVLHCHQGVVHRDLKPENLLASKCKGAALKADFLGLAIEVQGDQAWFGFAGTGY 180  
 Db 121 LESVNHCHQGVVHRDLKPENLLASKCKGAALKADFLGLAIEVQGDQAWFGFAGTGY 180  
 QY 181 LSPVLRKEAGKPVDMWAGVILYLLVGPFWDEDOHKLQIKAGAYDPPSPWDT 240  
 Db 181 LSPVLRKEAGKPVDMWAGVILYLLVGPFWDEDOHKLQIKAGAYDPPSPWDT 240  
 QY 241 VTPEAKNLINQMLTINPAKRITAEALKHPWCQRTSVASMMHROETVECLKFNARRKL 300  
 Db 241 VTPEAKNLINQMLTINPAKRITAEALKHPWCQRTSVASMMHROETVECLKFNARRKL 300  
 QY 301 KGAILTMTLATRNFS--VGRQTAPATMTAAAGTMTGLVQAKSLNKKADGVKPTQNS 358  
 Db 301 KGAILTMTLATRNFSKFTGR-----SMITKKGESQ----- 331  
 QY 359 TKNSAATSPKGTLPAPALEPQTVIHNVPDGIKSSDSANTTIEDDAK-ARKQETIKT 417  
 Db 332 -----VKSTDSSTILEDDEDDKARARQEIHKI 359  
 QY 418 TEQILAVNNGDFEAYA-----FYFENLAKNSKPIHTT 451  
 Db 418 TEQILAVNNGDFEAYA-----FYFENLAKNSKPIHTT 451  
 Db 418 TEQILAVNNGDFEAYA-----FYFENLAKNSKPIHTT 451

D0 360 TEQLEAINSDFGYTKICDPHLTAFEPEALGNLVEGIDFHKFFENVLGKNCKAINTT 419  
Qy 452 ILNPHVHVGEDAACTAYIRLTQYIDGGRPRTSQSEETRVVWHRDGGKQNVHFGCSGA 510  
D0 420 ILNPHVHLLGEARCIYVRLTQYIDKQGHATHQSEETRVVWHRDGGKQNVHFGHRSAS 478

Search completed: October 10, 2003, 08:08:03  
Job time : 87 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 10, 2003, 07:50:56 ; Search time 46 Seconds  
 (without alignments)  
 1078.762 Million cell updates/sec

Title: US-09-820-790B-2  
 Perfect score: 2715  
 Sequence: 1 MATTVTCTFRFTDEQLYEDI.....DGKNQNVHFCGAPVAPLQ 516

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_76:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2672	98.4	542	1 A45025	Ca2+/calmodulin-de
2	2669	98.3	542	1 A26464	Ca2+/calmodulin-de
3	2374.5	87.5	589	2 S68470	Ca2+/calmodulin-de
4	2250.5	82.9	527	1 A31908	Ca2+/calmodulin-de
5	2230	82.1	518	1 B46619	Ca2+/calmodulin-de
6	2216	81.6	518	1 S43845	Ca2+/calmodulin-de
7	2205	81.2	556	2 JC5636	Ca2+/calmodulin-de
8	2177	80.2	533	1 A34366	Ca2+/calmodulin-de
9	2012.5	74.1	478	1 A30355	Ca2+/calmodulin-de
10	1999.5	73.6	478	1 S04365	Ca2+/calmodulin-de
11	1861.5	68.6	516	1 U02720	Ca2+/calmodulin-de
12	1851	68.2	509	2 B44412	calmodulin-depnde
13	1840.5	67.8	530	2 D44412	Ca2+/calmodulin-de
14	1590.5	58.6	547	2 T23614	hypothetical prote
15	1501	55.3	708	2 T23616	hypothetical prote
16	633	23.3	474	1 TVRTC4	Ca2+/calmodulin-de
17	633	23.3	502	2 I52637	Ca2+/calmodulin-de
18	622	22.9	469	1 S17656	Ca2+/calmodulin-de
19	618.5	22.8	348	2 T37321	Ca2+/calmodulin-de
20	616	22.7	473	1 A53036	Ca2+/calmodulin-de
21	616	22.7	571	2 S69210	protein kinase cak
22	591	21.8	370	1 S50193	Ca2+/calmodulin-de
23	583	21.5	370	1 S57347	Ca2+/calmodulin-de
24	582.5	21.5	492	1 T03271	calcium-dependent
25	577	21.3	531	2 D85059	probable calcium d
26	576.5	21.2	556	2 T06126	calcium-dependent
27	575.5	21.2	554	1 T03263	calcium-stimulated
28	575	21.2	591	2 S54788	probable calmoduli
29	574.5	21.2	544	2 D84550	

30	573.5	21.1	532	2 T14335	protein kinase, ca
31	573	21.1	540	1 T01989	calcium-dependent
32	572	21.1	484	2 T05650	calcium-dependent
33	571	21.0	530	2 A84847	probable Ca2+ depe
34	566.5	20.9	495	1 S46284	calcium-dependent
35	565	20.8	490	2 T08873	calcium-dependent
36	563	20.7	533	1 S71778	calcium-dependent
37	561.5	20.7	501	2 G85097	hypothetical prote
38	561	20.7	521	2 G96543	calcium-dependent
39	558	20.6	508	1 A43713	calcium-dependent
40	558	20.6	533	1 S56652	calcium-dependent
41	557.5	20.5	553	1 T02139	calcium-dependent
42	557	20.5	554	2 T05476	calcium-dependent
43	556	20.5	310	2 B88540	protein K07A9.2 [i
44	555.5	20.5	487	1 S71770	calcium-dependent
45	555	20.4	538	2 T08874	calcium-dependent

## ALIGNMENTS

## RESULT 1

A45025  
 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) II beta chain - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 10-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 11-Jun-1999  
 C:Accession: A45025; S18915  
 R:Karis, U.; Muller, U.; Gilbert, D.J.; Copeland, N.G.; Jenkins, N.A.; Harbers, K.  
 Mol. Cell. Biol. 12, 3644-3652, 1992  
 A:Title: Structure, expression, and chromosome location of the gene for the beta s  
 nic lethal mouse mutant.  
 A:Reference number: A45025; MUID:92334366; PMID:1321343  
 A:Accession: A45025  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-542 <KAR>  
 A:Cross-references: GB:X63615; GB:S40077; NID:g50275; PIDN:CAA45160.1; PID:g50276  
 A:Experimental source: BALB/c, brain  
 A:Note: sequence inconsistent with the nucleotide translation  
 A:Note: sequence extracted from NCBI backbone (NCBIN:108750, NCBIPI:108751)  
 R:Karis, U.; Mueller, U.; Gilbert, D.J.; Copeland, N.G.; Jenkins, N.A.; Harbers, K  
 submitted to the EMBL Data Library, December 1991  
 A:Reference number: S18915  
 A:Accession: S18915  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-542 <KAR>  
 A:Cross-references: EMBL:X63615; NID:g50275; PIDN:CAA45160.1; PID:g50276  
 C:Complex: heteromultimer composed of 10-12 chains (alpha, beta, gamma, delta) gen  
 C:Function:  
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-th  
 A:Note: acts on a variety of intracellular proteins; alpha and beta chains are exp  
 C:Superfamily: Ca2+/calmodulin-dependent protein kinase II; protein kinase homolog  
 C:Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphot  
 F:12-272/Domain: protein kinase homology <KIN>  
 F:20-28/Region: protein kinase ATP-binding motif  
 F:287-311/Region: calmodulin binding #status predicted  
 F:43.61.136.138/Active site: Lys, Glu, Asp, Lys #status predicted  
 F:287/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pr

Query Match 98.4%; Score 2672; DB 1; Length 542;  
 Best Local Similarity 94.3%; Pred. No. 2.9e-112;  
 Matches 511; Conservative 3; Mismatches 2; Indels 26; Gaps 1;  
 QY 1 MATTVTCTFRFTDEQLYEDIKGAFSVWRCKVLCCTGHEVAAKTIINTKKLSARDHOKLER 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MATTVTCTFRFTDEQLYEDIKGAFSVWRCKVLCCTGHEVAAKTIINTKKLSARDHOKLER 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 61 EARICRLKHSNIVRLHDSISEGPHYLVDLVVTGGELFDIVAREYISEADASHCICQI 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 EARICRLKHSNIVRLHDSISEGPHYLVDLVVTGGELFDIVAREYISEADASHCICQI 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 121 LEAVLCHOMGVVHEDLKPENLLIASKGAANKLAFLGIAIEVQGDQAWFGAGTGY 180



Db 121 LEAVLHCHQMGVVRDLK?PENLLASKCKGAAVKLA?DGLAIEVQDQQA?WFGAGT?PGY 180  
 QY 181 LSPVLRKEAYGK?PVDI?WACGVILY?LLVGYPPFP?WDEDOH?KLYQOI?KAGAYD?PSP?EWD?T 240  
 Db 181 LSPVLRKEAYGK?PVDI?WACGVILY?LLVGYPPFP?WDEDOH?KLYQOI?KAGAYD?PSP?EWD?T 240  
 QY 241 VTPEAKNLINOMLTINPAKRITAEALKHPWVCQSTVASMHRQETVECLKFNARKL 300  
 Db 241 VTPEAKNLINOMLTINPAKRITAEALKHPWVCQSTVASMHRQETVECLKFNARKL 300  
 QY 301 KGAILTTMLATRNFSVGRQTTAPATMTAAAGTMTGLV?EQAKSLNKKADG?VKPQ?TNS?TK 360  
 Db 301 KGAILTTMLATRNFSVGRQTTAPATMTAAAGTMTGLV?EQAKSLNKKADG?VKPQ?TNS?TK 360  
 QY 361 NSAAATSPKGLPPAAL?EPQTTVIHNPVDG?IKESSDSANTTIEDEDAKARKQEI?IKTTEQ 420  
 Db 361 NSAAATSPKGLPPAAL?EPQTTVIHNPVDG?IKESSDSANTTIEDEDAKARKQEI?IKTTEQ 420  
 QY 421 LIEAVNNGDPEAVA-----FYFENLLAKNSKPIHTTILN 454  
 Db 421 LIEAVNNGDPEAVA-----FYFENLLAKNSKPIHTTILN 454  
 QY 455 PHVHVGIDDAACIAYIRLTQYIDGQGRPTSQSEETRVWHRDQKQWNVHFCSGAPVAP 514  
 Db 455 PHVHVGIDDAACIAYIRLTQYIDGQGRPTSQSEETRVWHRDQKQWNVHFCSGAPVAP 514  
 QY 515 LQ 516  
 Db 541 LQ 542

## RESULT 2

A26464  
 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) II beta chain - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 11-Jun-1999  
 C:Accession: A26464  
 R:Bennett, M.K.; Kennedy, M.B.  
 A:Title: Deduced primary structure of the beta-subunit of brain type II Ca(2+)/calmodulin  
 A:Reference number: A26464; MUID:87175563; PMID:3470758  
 A:Accession: A26464  
 A:Molecule type: mRNA  
 A:Residues: 1-542 <BN>  
 A:Cross-references: GB:X16112; NID:g206170; PIDN:AAA1866.1; PID:g206171  
 C:Complex: heteromultimer composed of 10-12 chains (alpha, beta, gamma, delta) generally  
 C:Function:  
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
 A:Note: acts on a variety of intracellular proteins; alpha and beta chains are expressed  
 C:Superfamily: Ca2+/calmodulin-dependent protein kinase II; protein kinase homology  
 C:Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotransfe  
 F:12-272/Domain: protein kinase homology <KIN>  
 F:20-28/Region: protein kinase ATP-binding motif  
 F:287-311/Region: calmodulin binding #status predicted  
 F:43,61,136,138/Active site: Lys, Glu, Asp, Lys #status predicted  
 F:287/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match 98.3%; Score 2669; DB 1; Length 542;  
 Best Local Similarity 94.3%; Pred. No. 3.9e-112;  
 Matches 511; Conservative 2; Mismatches 3; Indels 26; Gaps 1;

QY 1 MATTVCTRTFTDEYQIYEDIGKGFASVVRVCVKLTGHEYAALKIINTKKLSARDHOKLER 60  
 Db 1 MATTVCTRTFTDEYQIYEDIGKGFASVVRVCVKLTGHEYAALKIINTKKLSARDHOKLER 60  
 QY 61 EARICRLKHSNIVRLHDSISEEGFHYLVFDLVTGGELFEDIVAREYYSADASHCIQI 120  
 Db 61 EARICRLKHSNIVRLHDSISEEGFHYLVFDLVTGGELFEDIVAREYYSADASHCIQI 120  
 QY 121 LEAVLHCHQMGVVRDLK?PENLLASKCKGAAVKLA?DGLAIEVQDQQA?WFGAGT?PGY 180  
 Db 121 LEAVLHCHQMGVVRDLK?PENLLASKCKGAAVKLA?DGLAIEVQDQQA?WFGAGT?PGY 180

QY 181 LSPVLRKEAYGK?PVDI?WACGVILY?LLVGYPPFP?WDEDOH?KLYQOI?KAGAYD?PSP?EWD?T 240  
 Db 181 LSPVLRKEAYGK?PVDI?WACGVILY?LLVGYPPFP?WDEDOH?KLYQOI?KAGAYD?PSP?EWD?T 240  
 QY 241 VTPEAKNLINOMLTINPAKRITAEALKHPWVCQSTVASMHRQETVECLKFNARKL 300  
 Db 241 VTPEAKNLINOMLTINPAKRITAEALKHPWVCQSTVASMHRQETVECLKFNARKL 300  
 QY 301 KGAILTTMLATRNFSVGRQTTAPATMTAAAGTMTGLV?EQAKSLNKKADG?VKPQ?TNS?TK 360  
 Db 301 KGAILTTMLATRNFSVGRQTTAPATMTAAAGTMTGLV?EQAKSLNKKADG?VKPQ?TNS?TK 360  
 QY 361 NSAAATSPKGLPPAAL?EPQTTVIHNPVDG?IKESSDSANTTIEDEDAKARKQEI?IKTTEQ 420  
 Db 361 NSAAATSPKGLPPAAL?EPQTTVIHNPVDG?IKESSDSANTTIEDEDAKARKQEI?IKTTEQ 420  
 QY 421 LIEAVNNGDPEAVA-----FYFENLLAKNSKPIHTTILN 454  
 Db 421 LIEAVNNGDPEAVA-----FYFENLLAKNSKPIHTTILN 454  
 QY 455 PHVHVGIDDAACIAYIRLTQYIDGQGRPTSQSEETRVWHRDQKQWNVHFCSGAPVAP 514  
 Db 455 PHVHVGIDDAACIAYIRLTQYIDGQGRPTSQSEETRVWHRDQKQWNVHFCSGAPVAP 514  
 QY 515 LQ 516  
 Db 541 LQ 542

## RESULT 3

S68470  
 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) II beta-3 - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 18-Jun-1999  
 C:Accession: S68470; I33501  
 R:Orquid, V.; Aankroft, S.J.H.  
 F:85 Lett. 358, 23-26, 1995  
 A:Title: A novel pancreatic beta-cell isoform of calcium/calmodulin-dependent prote  
 A:Reference number: I33501; MUID:95121451; PMID:7821422  
 A:Accession: S68470  
 A:Molecule type: mRNA  
 A:Residues: 1-589 <URQ>  
 A:Cross-references: EMBL:X83375; NID:g603580; PIDN:CAA58289.1; PID:g603581  
 A:Experimental source: pancreatic islets  
 C:Complex: heteromultimer composed of 10-12 chains (alpha, beta, gamma, delta) gene  
 C:Superfamily: Ca2+/calmodulin-dependent protein kinase II; protein kinase homology  
 C:Keywords: alternative splicing; ATP; autophosphorylation; calmodulin binding; pho  
 F:12-272/Domain: protein kinase homology <KIN>  
 F:20-28/Region: protein kinase ATP-binding motif  
 F:287-311/Region: calmodulin binding #status predicted  
 F:43,61,136,138/Active site: Lys, Glu, Asp, Lys #status predicted  
 F:287/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status

Query Match 87.5%; Score 2374.5; DB 2; Length 589;  
 Best Local Similarity 75.0%; Pred. No. 5.4e-99;  
 Matches 471; Conservative 2; Mismatches 4; Indels 151; Gaps 4;

QY 1 MATTVCTRTFTDEYQIYEDIGKGFASVVRVCVKLTGHEYAALKIINTKKLSARDHOKLER 60  
 Db 1 MATTVCTRTFTDEYQIYEDIGKGFASVVRVCVKLTGHEYAALKIINTKKLSARDHOKLER 60  
 QY 61 EARICRLKHSNIVRLHDSISEEGFHYLVFDLVTGGELFEDIVAREYYSADASHCIQI 120  
 Db 61 EARICRLKHSNIVRLHDSISEEGFHYLVFDLVTGGELFEDIVAREYYSADASHCIQI 120  
 QY 121 LEAVLHCHQMGVVRDLK?PENLLASKCKGAAVKLA?DGLAIEVQDQQA?WFGAGT?PGY 180  
 Db 121 LEAVLHCHQMGVVRDLK?PENLLASKCKGAAVKLA?DGLAIEVQDQQA?WFGAGT?PGY 180  
 QY 181 LSPVLRKEAYGK?PVDI?WACGVILY?LLVGYPPFP?WDEDOH?KLYQOI?KAGAYD?PSP?EWD?T 240  
 Db 181 LSPVLRKEAYGK?PVDI?WACGVILY?LLVGYPPFP?WDEDOH?KLYQOI?KAGAYD?PSP?EWD?T 240

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QY 241 VTPEAKNLINOMLTINPAKRITAEALKHPWVQORSTVSMHMQETVECLKFNARRKL 300
DB 241 VTPEAKNLINOMLTINPAKRITAEALKHPWVQORSTVSMHMQETVECLKFNARRKL 300
QY 301 KGAILTMTLATRNFSVGRQTTAPAPMSTRAASGTMTGLVEQAKSLINKKADGKQTNSTK 360
DB 301 KGAILTMTLATRNFSVGRQTTAPAPMSTRAASGTMTGLVEQAKSLINKKADGKQTNSTK 360
QY 361 NSAAATSPKGLTPPAALPQTTVIHNPVDGKESDSANTTIEDDAKA----- 409
DB 361 NSAAATSPKGLTPPAALPQTTVIHNPVDGKESDSANTTIEDDAKA----- 409
QY 337 NSAAITSPKGLTPPAALPQTTVIHNPVDGKESDSANTTIEDDAKA----- 381
DB 337 NSAAITSPKGLTPPAALPQTTVIHNPVDGKESDSANTTIEDDAKA----- 381
QY 410 ----- 409
DB 410 ----- 409
QY 382 RGCQTPEAGPLSVGPPCLSPGLGPLTPSPRISDILNSVRSGSTPEAGLPPVGGP 441
DB 382 RGCQTPEAGPLSVGPPCLSPGLGPLTPSPRISDILNSVRSGSTPEAGLPPVGGP 441
QY 410 ----- 434
DB 410 ----- 434
QY 442 PCPSTPLGCLPPTSPKQELIKTEQLTEAVNNGDFEYAKICDPLGTSFPEALGNLVE 501
DB 442 PCPSTPLGCLPPTSPKQELIKTEQLTEAVNNGDFEYAKICDPLGTSFPEALGNLVE 501
QY 435 -----FFENLLAKNSKPTHTILNPHVHVGEDAAACIAYIRLTOYIDGQGRPTSSQSE 488
DB 435 -----FFENLLAKNSKPTHTILNPHVHVGEDAAACIAYIRLTOYIDGQGRPTSSQSE 488
QY 502 GMDPFRFVFNLLAKNSKPTHTILNPHVHVGEDAAACIAYIRLTOYIDGQGRPTSSQSE 561
DB 502 GMDPFRFVFNLLAKNSKPTHTILNPHVHVGEDAAACIAYIRLTOYIDGQGRPTSSQSE 561
QY 489 ETRVWHRDQKQWNVHFCSGAPVAPLQ 516
DB 489 ETRVWHRDQKQWNVHFCSGAPVAPLQ 516
QY 562 ETRVWHRDQKQWNVHFCSGAPVAPLQ 589
DB 562 ETRVWHRDQKQWNVHFCSGAPVAPLQ 589

RESULT 4
A31908
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) II gamma-a chain - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 11-Jun-1999
C:Accession: A31908
R:Tobimatsu, T.; Kaweshita, I.; Fujisawa, H.
J. Biol. Chem. 263, 16082-16086, 1988
A:Title: Molecular cloning of the cDNA encoding the third polypeptide (gamma) of brain c
A:Reference number: A31908; MUID:89034067; PMID:2846534
A:Accession: A31908
A:Molecule type: mRNA
A:Residues: 1-527 <TOS>
A:Cross-references: GB:J04063; NID:g206151; PID:AAA41857.1; PID:g206152
A:Experimental source: Jurkat T cells
A:Note: heteromultimer composed of 10-12 chains (alpha, beta, gamma, delta) generally
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A:Note: acts on a variety of intracellular proteins; gamma and delta chains are expresse
C:Superfamily: Ca2+/calmodulin-dependent protein kinase II; protein kinase homology
C:Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotransfe
F:12-272/Domain: protein kinase homology <KIN>
F:20-28/Region: protein kinase ATP-binding motif
F:287-311/Region: calmodulin binding #status predicted
F:43, 61, 136, 138/Active site: Lys, Glu, Asp, Lys #status predicted
F:287/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicte

Query Match 82.9%; Score 2250.5; DB 1; Length 527;
Best Local Similarity 79.7%; Pred. No. 1.6e-93;
Matches 433; Conservative 30; Mismatches 37; Indels 43; Gaps 4;

QY 1 MATVTTCFFDEVDYEDTGKGFSPVRCVKLCTGHEVAAKIINTKLSARDHOKLER 60
DB 1 MATATCTFTDVLDFEEIGKGFSPVRCVKKTSQEVAAKIINTKLSARDHOKLER 60

QY 61 EARICRLKHSNIVRLHDSISEGFFHYLFDLVTGGEFEDIVAREYISEADASHCICQI 120
DB 61 EARICRLKHPNIVRLHDSISEGFFHYLFDLVTGGEFEDIVAREYISEADASHCICQI 120

QY 121 LEAVLHCHQGVVHRLDKPNLLSKCKGAAGVAKLADFGIAIEVQGGQAWGFGAGTGGY 180
DB 121 LEAVNIHCHQGVVHRLDKPNLLSKCKGAAGVAKLADFGIAIEVQGGQAWGFGAGTGGY 180

QY 121 LESVNIHCHQGVVHRLDKPNLLSKCKGAAGVAKLADFGIAIEVQGGQAWGFGAGTGGY 180
DB 121 LESVNIHCHQGVVHRLDKPNLLSKCKGAAGVAKLADFGIAIEVQGGQAWGFGAGTGGY 180

QY 181 LSPFVLKRAYGKGVVDIHWACGVILYLLVGYPPFDEQHKLYQKIKAGAYDFPSPEDWT 240
DB 181 LSPFVLKRAYGKGVVDIHWACGVILYLLVGYPPFDEQHKLYQKIKAGAYDFPSPEDWT 240

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DB 181 LSPFVLKRAYGKGVVDIHWACGVILYLLVGYPPFDEQHKLYQKIKAGAYDFPSPEDWT 240
QY 241 VTPEAKNLINOMLTINPAKRITAEALKHPWVQORSTVSMHMQETVECLKFNARRKL 300
DB 241 VTPEAKNLINOMLTINPAKRITAEALKHPWVQORSTVSMHMQETVECLKFNARRKL 300
QY 301 KGAILTMTLATRNFSVGRQTTAPATNSTAASGTMTGLVEQAKSLINKKAD-GVKPOTNST 359
DB 301 KGAILTMTLATRNFSVGRQSSAPASAAAGLA---GQAAKSLINKKSDGGVYKKKSSS 357
QY 360 KNSAAATSPKGLTPPAALPQTTVIHNPVDGKESDSANTTIEDDAKAKOEIIKITE 419
DB 360 KNSAAATSPKGLTPPAALPQTTVIHNPVDGKESDSANTTIEDDAKAKOEIIKITE 419
QY 358 S-----VHLMPEQTIVVHNAVDGKESNTTIEDDLKYRKEIILKITE 404
DB 358 S-----VHLMPEQTIVVHNAVDGKESNTTIEDDLKYRKEIILKITE 404
QY 420 QLIEAVNNGDFEAYA-----FYFENLLAKNSKPIHTTIL 453
DB 420 QLIEAVNNGDFEAYTAKICDPLGTSFPEALGNLVEGMDPFKHFYFENLLSKNSKPIHTTIL 464
QY 454 NPHVHVGEDAAACIAYIRLTOYIDGQGRPTSSQSETRVWHRDQKQWNVHFCSGAPVA 513
DB 454 NPHVHVGEDAAACIAYIRLTOYIDGQGRPTSSQSETRVWHRDQKQWNVHFCSGAPVA 513
QY 465 NPHVHVGEDAAACIAYIRLTOYIDGQGRPTSSQSETRVWHRDQKQWNVHFCSGAPAA 524
DB 465 NPHVHVGEDAAACIAYIRLTOYIDGQGRPTSSQSETRVWHRDQKQWNVHFCSGAPAA 524
QY 514 PLQ 516
DB 514 PLQ 516
QY 525 PLQ 527
DB 525 PLQ 527

RESULT 5
B46619
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) II gamma chain, splice form
N:Contains: Ca2+/calmodulin-dependent protein kinase II gamma chain, splice form C
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
C:Accession: B46619; B46619; JC5637
R:Nghiem, P.; Saati, S.M.; Martens, C.L.; Gardner, P.; Schulman, H.
J. Biol. Chem. 268, 5471-5479, 1993
A:Title: Cloning and analysis of two new isoforms of multifunctional Ca2+/calmoduli
A:Reference number: A46619; MUID:93194838; PMID:8449910
A:Accession: B46619
A:Molecule type: mRNA
A:Residues: 1-518 <NGH1>
A:Cross-references: GB:L07044; NID:g291894
A:Experimental source: Jurkat T cells
A:Note: sequence extracted from NCBI backbone (NCBIN:127699, NCBI:P:127703)
A:Accession: A46619
A:Molecule type: mRNA
A:Residues: 1-330,354-518 <NGH2>
A:Cross-references: GB:L07043; NID:g291893
A:Experimental source: Jurkat T cells
A:Note: the sequence in GenBank entry HUMCCDPKA, release 103, (PID:g2204281) incorr
A:Note: sequence extracted from NCBI backbone (NCBIN:127696, NCBI:P:127698)
R:Breen, M.A.; Ashcroft, S.J.H.
Biochem. Biophys. Res. Commun. 236, 473-478, 1997
A:Title: Human islets of Langerhans express multiple isoforms of calcium/calmodulin
A:Reference number: JC5636; MUID:97382459; PMID:9240463
A:Accession: JC5637
A:Molecule type: mRNA
A:Residues: 1-384,386-518 <BRE>
A:Cross-references: GB:U66063
A:Experimental source: islet
C:Comment: This enzyme is a ubiquitous serine/threonine protein kinase. It plays a
C:Genetics:
A:Gene: GDB:CAMKG
A:Cross-references: GDB:138469
A:Map position: 10q22-10q22
C:Complex: heteromultimer composed of 10-12 alpha, beta, gamma, and delta chains ge
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-thr
A:Note: acts on a variety of intracellular proteins; gamma and delta chains are exp
C:Superfamily: Ca2+/calmodulin-dependent protein kinase II; protein kinase homology
C:Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotri
F:12-272/Domain: protein kinase homology <KIN>
F:20-28/Region: protein kinase homology <KIN>
F:287-311/Region: calmodulin binding #status predicted
F:43, 61, 136, 138/Active site: Lys, Glu, Asp, Lys #status predicted
F:287/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicte

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Query Match      81.2%; Score 2205; DB 2: Length 556;
Best Local Similarity 74.2%; Pred No. 1.8e-91;
Matches 431; Conservative 25; Mismatches 55; Indels 90; Gaps 5;

Qy 1 MATTVTCFRFDEYQLYEDIGKGAPSVWRRCVKLTGHEYAAKIINTKLSARDHQKLER 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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[illegible]

Db 1 MATTTATCTRTDYYQLFEELGKGAESVVRVCVKTSQEYAAKLIINTKKLSARDHQKLER 60  
 Qy 61 EARICRLKNSNIVRLHDSISEGPHYLVDLVGSELFDIVAREYYSEADASHCIQOI 120  
 Db 61 EARICRLKNSNIVRLHDSISEGPHYLVDLVGSELFDIVAREYYSEADASHCIQOI 120  
 Qy 121 LEAVLHCHQMGVYVHRDLKPNENLLASKCKGAAYKLADFGLAIEVQDQQAQFAGTPGY 180  
 Db 121 LEVNVHIIHQHDIHVRDLKPNENLLASKCKGAAYKLADFGLAIEVQDQQAQFAGTPGY 180  
 Qy 181 LSPEVLKREKXGKPVDIWACGVILYLLVGYPPFPWDDQKLYQQIKAGAYDFSPBWDI 240  
 Db 181 LSPEVLKXDPYKPVDIWACGVILYLLVGYPPFPWDDQKLYQQIKAGAYDFSPBWDI 240  
 Qy 241 VTPEAKNLINOMLTINPAKRITAEALKHPWVQORSTVASMHRQETVECLKFNARRKL 300  
 Db 241 VTPEAKNLINOMLTINPAKRITAEALKHPWVQORSTVASMHRQETVECLKFNARRKL 300  
 Qy 301 KGAILTTMLATRNFSVGRQTTAPATMSTAASGTTMGLVQAKSLNKKAD-GVKPOTNST 359  
 Db 301 KGAILTTMLATRNFSVGRQTTAPATMSTAASGTTMGLVQAKSLNKKAD-GVKPOTNST 359  
 Qy 360 KNSAATSPKGTLPALPEPQTVIHNPDGKIKSSDSANTTIEDAKA----- 409  
 Db 360 KNSAATSPKGTLPALPEPQTVIHNPDGKIKSSDSANTTIEDAKA----- 409  
 Qy 396 VPEGRSNDRTAPSGMQPQPSLCSAMRKQEIITKITEGLAINNGDFEAYTKICDPGL 455  
 Db 396 VPEGRSNDRTAPSGMQPQPSLCSAMRKQEIITKITEGLAINNGDFEAYTKICDPGL 455  
 Qy 435 -----FYFENLLAKNSKPIHTTILNPHVHVGEDAACTIATRLTQY 475  
 Db 435 -----FYFENLLAKNSKPIHTTILNPHVHVGEDAACTIATRLTQY 475  
 Qy 476 IDGGRPTSOSETRVWHRDQKWNVHFCSGAPVAPLQ 516  
 Db 516 IDGGRPTSOSETRVWHRDQKWNVHFCSGAPVAPLQ 556  
 RESULT 8  
 A34366  
 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) II delta chain - rat  
 N:Contains: Ca2+/calmodulin-dependent protein kinase II delta chain, various splice form  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 08-Jun-1990 #sequence, revision 08-Jun-1990 #text, change 11-Jun-1999  
 C:Accession: A34366; S39023; S39024; S39025; S39026; S39027; C47170  
 R:Tobinatsu, T.; Fujisawa, H.  
 J. Biol. Chem. 264, 17907-17912, 1989  
 A:Title: Tissue-specific expression of four types of rat calmodulin-dependent protein ki  
 A:Reference number: A34366; MUID:90036861; PMID:2553697  
 A:Accession: A34366  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-533 <TOR>  
 A:Cross-references: GB:J05072; NID:g203266; PIDN:AAA40866.1; PID:g203267  
 R:Mayex, P.; Moehlig, M.; Schatz, H.; Pfeiffer, A.  
 FEBS Lett. 333, 313-318, 1993  
 A:Title: New isoforms of multifunctional calcium/calmodulin-dependent protein kinase II.  
 A:Reference number: S39023; MUID:94039784; PMID:8224201  
 A:Accession: S39023  
 A:Molecule type: mRNA  
 A:Residues: 318-328, 363-371, 504-533 <MAY>  
 A:Accession: S39024  
 A:Molecule type: mRNA  
 A:Residues: 318-371, 504-511, 'N' <MA2>  
 A:Accession: S39025  
 A:Molecule type: mRNA  
 A:Residues: 318-328, 363-371, 504-511, 'N' <MA3>  
 A:Accession: S39026  
 A:Molecule type: mRNA  
 A:Residues: 318-349, 364-371, 504-533 <MA4>  
 A:Accession: S39027  
 A:Status: preliminary

A:Molecule type: mRNA  
 A:Residues: 318-349, 364-371, 504-511, 'N' <MA5>  
 R:Schworer, C.M.; Rothblum, L.I.; Thekkumkara, T.J.; Singer, H.A.  
 J. Biol. Chem. 268, 14443-14449, 1993  
 A:Title: Identification of novel isoforms of the delta subunit of Ca2+/calmodulin-d  
 A:Reference number: A47170; MUID:93300844; PMID:8390994  
 A:Accession: C47170  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 314-349, 364-368 <SCH>  
 A:Cross-references: GB:L13408; NID:g349086  
 A:Experimental source: skeletal muscle  
 A:Note: sequence extracted from NCBI backbone (NCBIN:134450, NCBI:P134453)  
 C:Complex: heteromultimer composed of 10-12 alpha, beta, gamma, and delta chains ge  
 C:Function:  
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-thr  
 A:Note: acts on a variety of intracellular proteins; gamma and delta chains are exp  
 C:Superfamily: Ca2+/calmodulin-dependent protein kinase II; protein kinase homology  
 C:Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotr  
 F:12-272/Domain: protein kinase homology <KIN>  
 F:20-28/Region: protein kinase ATP-binding motif  
 F:287-311/Region: calmodulin binding #status predicted  
 F:43,61,136,138/Active site: Lys, Glu, Asp, Lys #status predicted  
 F:287/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pre  
 Query Match 80.2%; Score 2177; DB 1; Length 533;  
 Best Local Similarity 77.5%; Pred No. 3e-90;  
 Matches 420; Conservative 31; Mismatches 35; Indels 56; Gaps 6;  
 Qy 1 MATTTCTRTDYYQLFEELGKGAESVVRVCVKTSQEYAAKLIINTKKLSARDHQKLER 60  
 Db 1 MATTTCTRTDYYQLFEELGKGAESVVRVCVKTSQEYAAKLIINTKKLSARDHQKLER 60  
 Qy 61 EARICRLKNSNIVRLHDSISEGPHYLVDLVGSELFDIVAREYYSEADASHCIQOI 120  
 Db 61 EARICRLKNSNIVRLHDSISEGPHYLVDLVGSELFDIVAREYYSEADASHCIQOI 120  
 Qy 121 LEAVLHCHQMGVYVHRDLKPNENLLASKCKGAAYKLADFGLAIEVQDQQAQFAGTPGY 180  
 Db 121 LEVNVHCHLNGIIVHRDLKPNENLLASKCKGAAYKLADFGLAIEVQDQQAQFAGTPGY 180  
 Qy 181 LSPEVLKREKXGKPVDIWACGVILYLLVGYPPFPWDDQKLYQQIKAGAYDFSPBWDI 240  
 Db 181 LSPEVLKXDPYKPVDIWACGVILYLLVGYPPFPWDDQKLYQQIKAGAYDFSPBWDI 240  
 Qy 241 VTPEAKNLINOMLTINPAKRITAEALKHPWVQORSTVASMHRQETVECLKFNARRKL 300  
 Db 241 VTPEAKNLINOMLTINPAKRITAEALKHPWVQORSTVASMHRQETVECLKFNARRKL 300  
 Qy 301 KGAILTTMLATRNFSVGRQTTAPATMSTAASGTTMGLVQAKSLNKKADGVKQPTNSTK 360  
 Db 301 KGAILTTMLATRNFSVGRQTTAPATMSTAASGTTMGLVQAKSLNKKADGVKQPTNSTK 360  
 Qy 361 NSAAATSPKGTLPALPEPQTVIHNPDGKIKSSDSANTTIEDAKARQEIITKTEQ 420  
 Db 361 NSAAATSPKGTLPALPEPQTVIHNPDGKIKSSDSANTTIEDAKARQEIITKTEQ 420  
 Qy 396 VPEGRSNDRTAPSGMQPQPSLCSAMRKQEIITKITEGLAINNGDFEAYTKICDPGL 455  
 Db 396 VPEGRSNDRTAPSGMQPQPSLCSAMRKQEIITKITEGLAINNGDFEAYTKICDPGL 455  
 Qy 421 LIEAVNNGDFEAYA-----FYFENLLAKNSKPIHTTILN 454  
 Db 421 LIEAVNNGDFEAYA-----FYFENLLAKNSKPIHTTILN 454  
 Qy 455 PHVHVGEDAACTIATRLTQYIDGGRPTSOSETRVWHRDQKWNVHFCSGAPVAP 514  
 Db 455 PHVHVGEDAACTIATRLTQYIDGGRPTSOSETRVWHRDQKWNVHFCSGAPVAP 514  
 Qy 515 LQ 516  
 Db 511 IK 512  
 RESULT 9  
 A30355  
 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) II alpha chain - rat

QY	64	ICRLKHSNIVRLHDSISEEGFHYLVFDLVTGGELFEDIVAREYISPADASHCIIQILEA	123
DB	63	ICRLKHPNIVRLHDSISEEGHHYLVFDLVTGGELFEDIVAREYISPADASHCIIQILEA	122
QY	124	VLHCHQGVVHRDLKPEKNILLASKKGAAYKADFLAGLAIEVGGQDAWFAGTGGYLSF	183
DB	123	VLHCHQGVVHRDLKPEKNILLASKKGAAYKADFLAGLAIEVEGGQDAWFAGTGGYLSF	182
QY	184	EVLKRAYKPYVDIWACGVILYILLVGYPPFWDSDOHKLYQQIKAGAYDFPSPENDVTTP	243
DB	183	EVLKRDYKPYVDIACGVILYILLVGYPPFWDSDQHRLYQQIKAGAYDFPSPENDVTTP	242
QY	244	EAKNLINQMILTNPAKRTAEBALKHPWVQCRSTVASMMHQETVECLKFPNARKLGA	303
DB	243	EAKDLINQMILTNPASKRTAEBALKHPWISHRSTVASCMSHQETVDCLKFPNARKLGA	302
QY	304	ILTTMLATRNFSVGRGTTAPATMTAASGTTMGLVBEQAKSLNKKADGVKPTQNSTKNSA	363
DB	303	ILTTMLATRNFSGG-----KSGGNKKNDGV-----	327
QY	364	AATSPKGTLPAALEPQTTVHNVPVDGIKESSDSANTTIEDAKAKQBIITTEQLIE	423
DB	328	-----KBSSESTNTTIEDDTKVRKQBIIVTTEQLIE	359
QY	424	AVNNGDFEAVA-----FYFENLLAKSKPHTHTILNPHV	457
DB	360	ALNSGDFFSTTKMCDPGMTAPEPALGNLVEGLDFRFFYFENLMSRNSKPVHTILNPHI	419
QY	458	HYIGEDAACIAYIRLTQYIDQGRPRTSQSESTRVWHRRDQKQWNVHFHCSGAP	511
DB	420	HLMGDSACIAYIRLTQYLDAGGIPRTAQSESTRVWHRRDQKQWIVHFHRSAGP	473

RESULT 10

S04365

Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) II alpha chain - mouse

N:Alternate names: CamKII alpha chain

C:Species: Mus musculus (house mouse)

C:Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 11-Jun-1999

C:Accession: S04365; S05279

R:Hanley, R.M.; Payne, M.E.; Cruzalegui, F.; Christenson, M.A.; Means, A.R.

Nucleic Acids Res. 17, 3992, 1989

A:Title: Sequence of the cDNA for the alpha subunit of calmodulin kinase II from mouse

A:Reference number: S04365; MUID:89282416; PMID:2543961

A:Accession: S04365

A:Molecule type: mRNA

A:Residues: 1-478 <HAN>

A:Cross-references: EMBL:X14836

R:Hanley, R.M.

submitted to the EMBL Data Library, March 1989

A:Reference number: S05279

A:Accession: S05279

A:Molecule type: mRNA

A:Residues: 1-39, 'P', 41-271, 'S', 273-478 <HA2>

A:Cross-references: EMBL:X14836; NID:950416; PIDN:CAA32946.1; PID:950417

C:Complex: heteromultimer composed of 10-12 chains (alpha, beta, gamma, delta) gener

C:Function:

A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-thre

A:Note: acts on a variety of intracellular proteins; alpha and beta chains are expre

C:Superfamily: Ca2+/calmodulin-dependent protein kinase II; protein kinase homology

C:Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotria

P:11-271/Domain: protein kinase homology <KIN>

P:13-271/Region: protein kinase ATP-binding motif

F:286-310/Region: calmodulin binding #status predicted

F:42,60,135,137/Active site: Lys, Glu, Asp, Lys #status predicted

F:286/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred

Query Match	73.6%	Score	1999.5	DB 1	Length	478			
Best Local Similarity	71.9%	Prod. No.	2.1e-92						
Matches	384	Conservative	33	Mismatches	28	Indels	89	Gaps	3

4

TVTCRTFDYQVLYEDIKGAFSVVRCVKLTCHGYAAKIINTKKLSARDHOKLFEAR

63

[illegible]

RESULT 12  
B44412  
calmodulin-dependent protein kinase II (EC 2.7.1.-), 57.6K splice form - fruit fly  
C:Species: Drosophila melanogaster  
C:Date: 30-Apr-1993 #sequence\_revision 30-Apr-1993 #text\_change 10-Jul-1998  
C:Accession: B44412  
R:Ohsako, S.; Nishida, Y.; Ryo, H.; Yamauchi, T.  
J. Biol. Chem. 268, 2052-2062, 1993  
A:Title: Molecular characterization and expression of the Drosophila Ca2+/calmodulin  
native splicing.  
A:Reference number: A44412; PMID:93131962; PMID:8380587  
A:Contents: head  
A:Accession: B44412  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-509 <OHS>

[illegible]



Search completed: October 10, 2003, 08:11:31  
Job time : 48 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 10, 2003, 06:30:15 ; Search time 23 Seconds  
(without alignments)  
1055.034 Million cell updates/sec

Title: US-09-820-790B-2

Sequence: 1 MATIVICTRFTDEYQLYEDI.....DGKQNVHPCSGAPVAPLQ 516

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2672	98.4	542	1 KCCB_MOUSE	P28652 mus musculus
2	2669	98.3	542	1 KCCB_RAT	P08413 rattus norv
3	2631	96.5	664	1 KCCB_HUMAN	Q13554 homo sapien
4	2250.5	82.9	527	1 KCCG_RAT	P11730 rattus norv
5	2215.5	81.6	529	1 KCCG_MOUSE	Q92319 mus musculus
6	2177	80.2	533	1 KCCD_RAT	P15791 rattus norv
7	2070	76.2	499	1 KCCD_HUMAN	P13557 homo sapien
8	2012.5	74.1	478	1 KCCA_RAT	P11275 rattus norv
9	2008.5	74.0	478	1 KCCA_HUMAN	Q9ugm7 homo sapien
10	1994.5	73.5	478	1 KCCG_MOUSE	P11798 mus musculus
11	1872.5	69.0	472	1 KCCG_HUMAN	Q13555 homo sapien
12	736	27.1	926	1 CSKP_HUMAN	O14936 homo sapien
13	725.5	26.7	909	1 CSKP_RAT	Q62915 rattus norv
14	725	26.7	924	1 CSKP_MOUSE	O70589 mus musculus
15	633	23.3	474	1 KCC4_RAT	P13234 rattus norv
16	622	22.9	469	1 KCC4_MOUSE	P08414 mus musculus
17	616	22.7	473	1 KCC4_HUMAN	Q16566 homo sapien
18	611	22.5	897	1 CAKI_DROME	Q24210 drosophila
19	591	21.8	374	1 KCC1_RAT	O63450 rattus norv
20	587	21.6	374	1 KCC1_MOUSE	Q91yvs8 mus musculus
21	583	21.5	370	1 KCC1_HUMAN	Q14012 homo sapien
22	583	21.5	433	1 DCK1_RAT	O08875 rattus norv
23	583	21.5	756	1 DCK1_MOUSE	Q9j1m8 mus musculus
24	573.5	21.1	532	1 CDPK_DAUCA	P28582 daucus caro
25	572	21.1	740	1 DCK1_HUMAN	O15075 homo sapien
26	558	20.6	508	1 CDPK_SOYBN	P28583 glycine max
27	558	20.6	533	1 CDP2_ORYSA	P53683 oryza sativ
28	549.5	20.2	424	1 KPSE_HUMAN	P11801 homo sapien
29	549	20.2	406	1 KPBE_HUMAN	P15735 homo sapien
30	548	20.2	295	1 KMLC_DICDI	P25323 dictyosteli
31	547.5	20.2	534	1 CDP1_ORYSA	P53682 oryza sativ
32	546	20.1	542	1 CDP3_ORYSA	P53684 oryza sativ
33	535.5	19.7	513	1 CDP2_MAIZE	P49101 zea mays (m

#### RESULT 1

KCCB_MOUSE					
ID	KCCB_MOUSE	STANDARD;	PRT;	542 AA.	
AC	P28652;				
DT	01-DEC-1992 (Rel. 24, Created)				
DT	01-DEC-1992 (Rel. 24, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Calcium/calmodulin-dependent protein kinase type II beta chain				
DE	(EC 2.7.1.123) (CaM-kinase II beta chain) (CaM kinase II beta subunit)				
DE	(CaM-kinase II beta subunit).				
GN	CaMK2B.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BALE/c; TISSUE=Brain;				
RX	MEDLINE=92334366; PubMed=1321343;				
RA	Karls U., Mueller U., Gilbert D.J., Copeland N.G., Jenkins N.A.,				
RA	Harbers K.;				
RT	"Structure, expression, and chromosome location of the gene for the				
RT	beta subunit of brain-specific Ca2+/calmodulin-dependent protein				
RT	kinase II identified by transgene integration in an embryonic lethal				
RT	mouse mutant.";				
RL	Mol. Cell. Biol. 12:3644-3652(1992).				
CC	-I- FUNCTION: THIS KINASE MAY PLAY A ROLE IN NEUROTRANSMISSION.				
CC	-I- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.				
CC	-I- ENZYME REGULATION: AUTOPHOSPHORYLATION OF CaM-KINASE II PLAYS AN				
CC	IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.				
CC	-I- SUBUNIT: COMPOSED OF FOUR DIFFERENT CHAINS: ALPHA, BETA, GAMMA,				
CC	AND DELTA.				
CC	-I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.				
CC	CAMK SUBFAMILY.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
CC	EMBL; X63615; CAA45160.1; -				
DR	PIR; A45025; A45025.				
DR	HSP; Q63450; IA06.				
DR	MGI; 88257; Camk2b.				
DR	InterPro; IPR000719; Prot_kinase.				
DR	InterPro; IPR002290; Ser_thr_kinase.				
DR	Pfam; PF00069; pkinase; 1				
DR	ProDom; PD000001; Prot_kinase; 1				
DR	SMART; SM00220; S_Trc; 1.				
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.				
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.				
DR	PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.				
DR	Transferase; Serine/threonine-protein kinase; Calmodulin-binding;				
KW					

Q9db30 mus musculus  
P22517 saccharomyc  
Q06850 arabidopsis  
P00518 oryctolagus  
O42844 schizosacch  
Q16816 homo sapien  
P13325 rattus norv  
P13286 rattus norv  
O94547 schizosacch  
P07934 mus musculus  
Q38997 arabidopsis  
Q15349 homo sapien

#### ALIGNMENTS

```

KW Phosphorylation; ATP-binding; Neurone.
FT DOMAIN 14 272 PROTEIN KINASE.
FT NP_BIND 20 28 ATP (BY SIMILARITY).
FT BINDING 43 43 ATP (BY SIMILARITY).
FT ACT_SITE 136 136 BY SIMILARITY.
FT DOMAIN 291 301 CALMODULIN-BINDING.
SQ SEQUENCE 542 AA; 60475 MW; 8A7962A62D7075D0 CRC64;

Query Match 98.4%; Score 2672; DB 1; Length 542;
Best Local Similarity 94.3%; Pred. No. 8.2e-164;
Matches 511; Conservative 3; Mismatches 2; Indels 26; Gaps 1;

QY 1 MATVTCTRTDEYLYEDIGKGFVVRVRCVKLCTGHEYAAKIINTKKLSARDHOKLER 60
DB 1 MATVTCTRTDEYLYEDIGKGFVVRVRCVKLCTGHEYAAKIINTKKLSARDHOKLER 60
QY 61 EARICRLKHSNIVRLHDSISEGFGHYLVFDLVGTGSELPEDIVAREYSEADASHCIIQI 120
DB 61 EARICRLKHSNIVRLHDSISEGFGHYLVFDLVGTGSELPEDIVAREYSEADASHCIIQI 120
QY 121 LEAVLHCHQGVVHRDLKPNELLASKCKGAAYKVLADFGLAIEVQDQQAQWFGAGTGGY 180
DB 121 LEAVLHCHQGVVHRDLKPNELLASKCKGAAYKVLADFGLAIEVQDQQAQWFGAGTGGY 180
QY 181 LSPVLRKEAYGKPVDIWACGVILYLLVGPFPFDEDOHKLYQOIKAGAYDFPSPEDWT 240
DB 181 LSPVLRKEAYGKPVDIWACGVILYLLVGPFPFDEDOHKLYQOIKAGAYDFPSPEDWT 240
QY 241 VTPKAKLINQMLTINPAKRIKTHAELKHPWCQRTVASMHRQETVECLKKFNARRKL 300
DB 241 VTPKAKLINQMLTINPAKRIKTHAELKHPWCQRTVASMHRQETVECLKKFNARRKL 300
QY 301 KGAILTTMLATRNFSVGRQTAPATMSTAASGTTMGLVEQAKSLNKKADGVKVPQTNSTK 360
DB 301 KGAILTTMLATRNFSVGRQTAPATMSTAASGTTMGLVEQAKSLNKKADGVKVPQTNSTK 360
QY 361 NSAAATSPKGLTPPAALEPQTTVHNPDVGIKESSDSTNTTIEDDAKARKQEIITKTEQ 420
DB 361 NSAAATSPKGLTPPAALEPQTTVHNPDVGIKESSDSTNTTIEDDAKARKQEIITKTEQ 420
QY 421 LIEAVNGDPEAYA-----FYFENLLAKNSKPIHTIILN 454
DB 421 LIEAVNGDPEAYA-----FYFENLLAKNSKPIHTIILN 454
QY 455 PHVHVGEDAACTAYIRLTQYIDGGRPRTSQSEETRVVWHRDQKQWNVHFGHSGAPVAP 514
DB 455 PHVHVGEDAACTAYIRLTQYIDGGRPRTSQSEETRVVWHRDQKQWNVHFGHSGAPVAP 514
QY 515 LQ 516
DB 541 LQ 542

RESULT 2
KCCB_RAT
ID KCCB_RAT STANDARD; PRT; 542 AA.
AC P08413;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type II beta chain
DE (EC 2.7.1.123) (CaM-kinase II beta chain) (CaM kinase II beta subunit)
DE (CaM-K-II beta subunit).
GN CAMK2B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=87175563; PubMed=3470758;
RA Bennett M.K., Kennedy M.B.;

```

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RT "Deduced primary structure of the beta subunit of brain type II
RT Ca2+/calmodulin-dependent protein kinase determined by molecular
RT cloning.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:1794-1798(1987).
CC -!- FUNCTION: THIS KINASE MAY PLAY A ROLE IN NEUROTRANSMISSION.
CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -!- ENZYME REGULATION: AUTOPHOSPHORYLATION OF CAM-KINASE II PLAYS AN
CC IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
CC -!- SUBUNIT: COMPOSED OF FOUR DIFFERENT CHAINS: ALPHA, BETA, GAMMA,
CC AND DELTA.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC EMBL: M16112; AAA41866.1;
CC PIR: A26464; A26464.
CC HSP: Q63450; I806.
CC InterPro: IPR000719; Prot_Kinase.
CC InterPro: IPR002290; Ser_thr_kinase.
CC Pfam: PF00069; pkinase; 1.
CC ProDom: PD000001; Prot_kinase; 1.
CC SMART: SM00220; S_TKc; 1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
CC KW Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
CC Phosphorylation; ATP-binding; Neurone.
CC DOMAIN 14 272 PROTEIN KINASE.
CC NP_BIND 20 28 ATP (BY SIMILARITY).
CC BINDING 43 43 ATP (BY SIMILARITY).
CC ACT_SITE 136 136 BY SIMILARITY.
CC DOMAIN 291 301 CALMODULIN-BINDING.
SQ SEQUENCE 542 AA; 60401 MW; 8A7962A6A930D0 CRC64;

Query Match 98.3%; Score 2669; DB 1; Length 542;
Best Local Similarity 94.3%; Pred. No. 1.3e-163;
Matches 511; Conservative 2; Mismatches 3; Indels 26; Gaps 1;

QY 1 MATVTCTRTDEYLYEDIGKGFVVRVRCVKLCTGHEYAAKIINTKKLSARDHOKLER 60
DB 1 MATVTCTRTDEYLYEDIGKGFVVRVRCVKLCTGHEYAAKIINTKKLSARDHOKLER 60
QY 61 EARICRLKHSNIVRLHDSISEGFGHYLVFDLVGTGSELPEDIVAREYSEADASHCIIQI 120
DB 61 EARICRLKHSNIVRLHDSISEGFGHYLVFDLVGTGSELPEDIVAREYSEADASHCIIQI 120
QY 121 LEAVLHCHQGVVHRDLKPNELLASKCKGAAYKVLADFGLAIEVQDQQAQWFGAGTGGY 180
DB 121 LEAVLHCHQGVVHRDLKPNELLASKCKGAAYKVLADFGLAIEVQDQQAQWFGAGTGGY 180
QY 181 LSPVLRKEAYGKPVDIWACGVILYLLVGPFPFDEDOHKLYQOIKAGAYDFPSPEDWT 240
DB 181 LSPVLRKEAYGKPVDIWACGVILYLLVGPFPFDEDOHKLYQOIKAGAYDFPSPEDWT 240
QY 241 VTPKAKLINQMLTINPAKRIKTHAELKHPWCQRTVASMHRQETVECLKKFNARRKL 300
DB 241 VTPKAKLINQMLTINPAKRIKTHAELKHPWCQRTVASMHRQETVECLKKFNARRKL 300
QY 301 KGAILTTMLATRNFSVGRQTAPATMSTAASGTTMGLVEQAKSLNKKADGVKVPQTNSTK 360
DB 301 KGAILTTMLATRNFSVGRQTAPATMSTAASGTTMGLVEQAKSLNKKADGVKVPQTNSTK 360
QY 361 NSAAATSPKGLTPPAALEPQTTVHNPDVGIKESSDSTNTTIEDDAKARKQEIITKTEQ 420
DB 361 NSAAATSPKGLTPPAALEPQTTVHNPDVGIKESSDSTNTTIEDDAKARKQEIITKTEQ 420

```



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FT      3. isoform 5, isoform 6 and isoform 7}.
FT      /FTid=VSP_004776.
FT      Missing (in isoform 6).
FT      /FTid=VSP_004777.
FT      L -> V (IN REF. 3).
FT      K -> N (IN REF. 5).
FT      664 AA; 72726 MW; 98C82918D986814 CRC64;
SQ      SEQUENCE

Query Match      96.5%; Score 2621; DB 1; Length 664;
Best Local Similarity 77.7%; Pred. No. 1.9e-160;
Matches 516; Conservative 0; Mismatches 0; Indels 148; Gaps 2;

QY      1 MATTVTCTFRFDEQYLEDIGKAFSVVRCVKLCTGHEYAAKIINTKKLSARDHOKLER 60
DB      1 MATTVTCTFRFDEQYLEDIGKAFSVVRCVKLCTGHEYAAKIINTKKLSARDHOKLER 60
QY      61 EARIKLLKHSNIVRLHDSISEGPHYLVDLVLTGGELFEDIVAREYTYSEADASHCTQOI 120
DB      61 EARIKLLKHSNIVRLHDSISEGPHYLVDLVLTGGELFEDIVAREYTYSEADASHCTQOI 120
QY      121 LEAVLHCHQGVVHRDLKPENLLASKCKGAAYKLADFGLAIEVGDQQAWEFGAGTGGY 180
DB      121 LEAVLHCHQGVVHRDLKPENLLASKCKGAAYKLADFGLAIEVGDQQAWEFGAGTGGY 180
QY      181 LSPEYLKRAYKGPVDIACGVLYLLVGYPPFWDQDKLYQQIKAGAYDFPSPEDWT 240
DB      181 LSPEYLKRAYKGPVDIACGVLYLLVGYPPFWDQDKLYQQIKAGAYDFPSPEDWT 240
QY      241 VTPKAKLINOMLTINPAKRITAEALHPWVQORSTVASMHRQETVECLKKNAREKL 300
DB      241 VTPKAKLINOMLTINPAKRITAEALHPWVQORSTVASMHRQETVECLKKNAREKL 300
QY      301 KGAILTTMLATRNFSVGROTTAPATMSTAASGTTMGLVEQAKSLNKKADGVKQTNSTK 360
DB      301 KGAILTTMLATRNFSVGROTTAPATMSTAASGTTMGLVEQAKSLNKKADGVKQTNSTK 360
QY      361 NSAAATSPKGLPAALEPQTTVIHNPVDGIKESSDSANTTIEDAKA----- 409
DB      361 NSAAATSPKGLPAALEPQTTVIHNPVDGIKESSDSANTTIEDAKAPRPDILSSVR 420
QY      410 ----- 409
DB      421 RSGARSRGAPACSPAPSPILPAPSPRISDILNSVGRSGTPEAGPLSRGPPCLSPA 480
QY      410 -----RKQEIITKT 418
DB      481 LKGPLSPSPRISDILNSVGRSGTPEAEAPROWPPPCSPPTPGPLTPSRKQEIITKT 540
QY      419 EQLIEAVNNGDFEAYA-----FYFENLLAKNSKPIHTTI 452
DB      541 EQLIEAVNNGDFEAYAKICDGLTSPFEALGNLVEGMDHFRFYFENLLAKNSKPIHTTI 600
QY      453 LNPVHVIGEDACIAYIRLTQYIDQGRPRTSQSEETRVWHRDCKQWNVHFCSGAPV 512
DB      601 LNPVHVIGEDACIAYIRLTQYIDQGRPRTSQSEETRVWHRDCKQWNVHFCSGAPV 660
QY      513 APLQ 516
DB      661 APLQ 664

RESULT 4
ID      KCCG_RAT
AC      P11730; Q64003; Q64004;
DT      01-OCT-1989 (Rel. 12, Created)
DT      28-FEB-2003 (Rel. 12, Last sequence update)
DE      Calcium/calmodulin-dependent protein kinase type II gamma chain
DE      (EC 2.7.1.123) (CaM-kinase II gamma chain) (CaM kinase II gamma
DE      subunit) (CaM-II gamma subunit).
GN      CAMK2G.
OS      Rattus norvegicus (Rat).

```

```

CC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORM A).
RC      TISSUE=Brain;
RX      MEDLINE=89034067; PubMed=2846534;
RA      Tobimatsu T., Kameshita I., Fujisawa H.;
RT      Molecular cloning of the cDNA encoding the third polypeptide (gamma)
RT      of brain calmodulin-dependent protein kinase II.;
RL      J. Biol. Chem. 263:16082-16086(1988).
RN      [2]
RP      SEQUENCE FROM N.A. (ISOFORMS B AND C).
RC      TISSUE=Aortic smooth muscle;
RX      MEDLINE=94226614; PubMed=8172610;
RA      Zhou Z.-L., Ikebe M.;
RT      'New isoforms of Ca2+/calmodulin-dependent protein kinase II in
RT      smooth muscle.';
RL      Biochem. J. 293:489-495(1994).
CC      !- FUNCTION: THIS KINASE MAY PLAY A ROLE IN NEUROTRANSMISSION.
CC      !- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC      !- ENZYME REGULATION: AUTOPHOSPHORYLATION OF CAM-KINASE II PLAYS AN
CC      IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
CC      !- SUBUNIT: COMPOSED OF FOUR DIFFERENT CHAINS: ALPHA, BETA, GAMMA,
CC      AND DELTA.
CC      !- ALTERNATIVE PRODUCTS:
CC      Event-Alternative splicing; Named isoforms=3;
CC      Comment=Additional isoforms seem to exist;
CC      Name=A;
CC      IsoId=P11730-1; Sequence=Displayed;
CC      Name=B;
CC      IsoId=P11730-2; Sequence=VSP_004781, VSP_004782;
CC      Name=C;
CC      IsoId=P11730-3; Sequence=VSP_004781, VSP_004783;
CC      !- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CAMK
CC      SUBFAMILY.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch)).
CC      -----
CC      EMBL; J04063; AAA1857.1; .
DR      EMBL; S71570; AAB30670.1; .
DR      EMBL; S71571; AAB30671.1; .
DR      PIR; A31908; A31908.
DR      HSP; Q63450; 1A06.
DR      InterPro; IPR000719; Prot_kinase.
DR      InterPro; IPR002290; Ser_thr_kinase.
DR      Pfam; PF00069; pkinase; 1.
DR      ProDom; PD000001; Prot_kinase; 1.
DR      SMART; SM00220; S_TKc; 1.
DR      PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR      PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR      PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW      Phosphorylation; ATP-binding; Neurone; Alternative splicing.
FT      DOMAIN 14 272 PROTEIN KINASE.
FT      BINDING 20 28 ATP (BY SIMILARITY).
FT      ACT_SITE 136 136 ATP (BY SIMILARITY).
FT      DOMAIN 291 301 CALMODULIN-BINDING (BY SIMILARITY).
FT      VARSPPLIC 316 336 Missing (in isoform B and isoform C).
FT      FTid=VSP_004781.
FT      VARSPLIC 351 361 KKRKSSSVHL -> PEQQQKSRKSPRARQPLQTA (in
FT      isoform B).
FT      FTid=VSP_004782.
FT      VARSPLIC 352 362 Missing (in isoform C).
FT      FTid=VSP_004783.
FT      CONFLICT 2 2 A -> E (IN REF. 2).

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SQ SEQUENCE 527 AA; 59038 MW; 58DBF1B72F64FA31 CRC64;
Query Match 82.9%; Score 2250.5; DB 1; Length 527;
Best Local Similarity 79.7%; Pred. No. 7.3e-137;
Matches 433; Conservative 30; Mismatches 37; Indels 43; Gaps 4;

QY 1 MATTTCTRTDTEYDYGKAFSVVRRVCVKLCTGHEYAAXIINTKLSARDHOKLER 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MATTTATCTRTDDYQYFEEELGKAFSVVRRVCVKTSQYEAAXIINTKLSARDHOKLER 60

QY 61 EARIICRLKISNIVRLHDSISEGPHYLVFLVLTGGELFEDIVARYSEADASHCICQI 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 EARIICRLKPNIVRLHDSISEGPHYLVFLVLTGGELFEDIVAREYSEADASHCICQI 120

QY 121 LEAVLHCHGVVHRLDKPENILLASKCKGAAGVLADEGLAIEVQDQAGFAGTGGY 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 LESVNHVHQHDIIVHRLDKPENILLASKCKGAAGVLADEGLAIEVQEQAGFAGTGGY 180

QY 181 LSPVLKREAYGKVPDIWACGVILYLVGYPFPFWDSDQHKLYQIKAGAYDFSPWDI 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 LSPVLKRDYKVPDIWACGVILYLVGYPFPFWDSDQHKLYQIKAGAYDFSPWDI 240

QY 241 VTPAKNLINQMLTINPAKRIYAHALKHPVVCORSTVASMMHROBTVECLKKNARKL 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 VTPAKNLINQMLTINPAKRIYADQALKHPVVCORSTVASMMHROBTVECLKKNARKL 300

QY 301 KGAILTTMLATRNFSVGROTTAPATMTAAAGTTMGLVEQAKSLNKKAD-GYKPOTNST 359
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 301 KGAILTMYLVRNFSVGRSSAPASPAASAGLA---GQAASLNLKNSDGVYKRRKSS 357

QY 360 KNSAAATSPKGLTPAALSPQTVTHNPVDGKESDSANTTIEDDAKARKQEIIRKTE 419
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 360 S-----VHLMFPQTVVHNATDGIKSTESCNTTDEDLKVRKQEIIRKTE 404

QY 420 OLIEAVNNGDFEAYA-----FFENLLAKNSKPIHTIIL 453
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 405 QLIEAINNGDFEAYTIKIDPGLTSPFEALGNLVEGMDFFKFFENLLSKNSKPIHTIIL 464

QY 454 NPHVHVIGEDAAICAIYIRLTQYIDGGPRPTSQSEETRVVHRDQKQWVHFGSGAPVA 513
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 465 NPHVHVIGEDAAICAIYIRLTQYIDGGPRPTSQSEETRVVHRDQKQWVHFGSGAPAA 524

QY 514 PLQ 516
   |||
Db 525 PLQ 527

RESULT 5
KCCG_MOUSE STANDARD; PRT; 529 AA.
AC Q923T9; Q8VBD3;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 42, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type II gamma chain
DE (EC 2.7.1.123) (CaM-kinase II gamma chain) (Cam kinase II gamma
DE subunit) (CaM-k II gamma subunit).
DN CAMK2G.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RC SPRAIN=C57BL/6;
RA Scordo P.I.; Cadenas C.; Eichele G.;
RT "Identification of a mouse Ca2+/calmodulin-dependent protein kinase
RT II."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.,
   4;
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QY 304 ILTMTLATRNFSVGRQTTPATMTASTAASGTTMGLVEQAKSLNKKADGKVPQTNSTKNSA 363
Db 303 ILTMTLATRNFSGG-----KSGGKNKNDGV-----327
QY 364 AATSPKGLTPAALPQTTVIHNPVDGKESDSANTTIEDAKARKOEIKTTEQLIE 423
Db 328 -----KESSESTNTTIEDTKVKOEIKTTEQLIE 359
QY 424 AVNNGDFEAYA-----FYFENLLAKNSKPIHTTILNPHV 457
Db 360 AINSNGGFESYTKMCDPGMTAFEPALGNLVEGLDFHRFYFENLWSRNSKPVHTTILNPHI 419
QY 458 HVGIEDAACIAYIRLTOYIDGGRPTSQSEETRWHRDQKQWNVHFCSCGAP 511
Db 420 HLMGDESACIAYIRITQYILDAGGIPRTAQSEETRWHRDQKQWIVHFRSGAP 473

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## RESULT 9

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KCCA_HUMAN
ID KCCA_HUMAN STANDARD; PRT: 478 AA.
AC Q9UQM7; Q9Y352;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Calcium/calmodulin-dependent protein kinase type II alpha chain
DE (EC 2.7.1.123) (CaM-kinase II alpha chain) (CaM kinase II alpha
DE subunit) (CaM-II alpha subunit).
GN CAMK2A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RC TISSUE=Brain;
RA Li G.Y., Cooper N.G.F.;
RT "Human calcium/calmodulin-dependent protein kinase II: cDNA cloning
RT and gene analysis.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS KINASE MAY PLAY A ROLE IN NEUROTRANSMISSION.
CC -1- CATALYTIC ACTIVITY: ATP + protein -> ADP + O-phosphoprotein.
CC -1- ENZYME REGULATION: Autophosphorylation of Thr-286 allows the
CC kinase to switch from a calmodulin-dependent to a calmodulin-
CC independent state (By similarity).
CC -1- SUBUNIT: COMPOSED OF FOUR DIFFERENT CHAINS: ALPHA, BETA, GAMMA,
CC AND DELTA.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=alternative splicing; Named isoforms=2;
CC Name=A;
CC Name=B;
CC IsoId=Q9UQM7-1; Sequence=Displayed;
CC IsoId=Q9UQM7-2; Sequence=VSP_004766;
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CAMK
CC SUBFAMILY.

```

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```

CC -----
CC EMBL; AF145710; AAD30558.1; -
CC DR EMBL; AF145711; AAD30559.1; -
CC DR HSP; Q63450; 1A06.
CC Genew; HGNC:1460; CAMK2A.
CC MIM; 114078; -
CC InterPro; IPR000719; Prot_kinase.
CC DR InterPro; IPR002290; Ser_thr_kinase.
CC DR Pfam; PF00069; pkinase; 1.
CC DR ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00220; S_TFC; 1.

```

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DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW Phosphorylation; ATP-binding; Alternative splicing.
FT DOMAIN 13 271 PROTEIN_KINASE.
FT NP_BIND 19 27 ATP (BY SIMILARITY).
FT BINDING 42 42 ATP (BY SIMILARITY).
FT ACT_SITE 135 135 BY SIMILARITY.
FT MOD_RES 286 286 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT DOMAIN 290 300 CALMODULIN-BINDING.
FT VARSPLIC 328 328 K -> KKRKSSSSVQLM (in isoform B).
FT FTID=VSP_004766.
SQ SEQUENCE 478 AA; 54029 MW; 10800A85CAD724BB CRC64;

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Query Match 74.08; Score 2008.5; DB 1; Length 478;

Best Local Similarity 72.18; Pred. No. 2e-121;  
Matches 385; Conservative 34; Mismatches 26; Indels 89; Gaps 3;

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QY 4 TVTCTRTFDYDLYEDIGKAFSVVRCVKLCTGHEYAAKIINTKLSARDHOKLEREAR 63
Db 3 TTTCIRFTFEYQLFEELGKGFVSVRCVKLAGOETAAKIINTKLSARDHOKLEREAR 62
QY 64 ICRLLKHSNIVRLHDSISEEGFYHVLFDLVTGGELFEDIIVAREYYSEADASHCIQILEA 123
Db 63 ICRLLKHSNIVRLHDSISEEGHYHFLFDLVTGGELFEDIIVAREYYSEADASHCIQILEA 122
QY 124 VLHCHQMGVHRDLKPEENLLASKCKGAAYKLADFLGIAIEVQDQQAQWFGAGPYGLSP 183
Db 123 VLHCHQMGVHRDLKPEENLLASKLKGAAVKLADFLGIAIEVEGEQAQWFGAGPYGLSP 182
QY 184 EYLRKEAYGKPDVLIWAGGVILILLVGYPPFWDSDQKLYQQLKAGAYDFPSPWDVTVP 243
Db 183 EVLRKDPYKPKVDLWAGGVILILLVGYPPFWDSDQKLYQQLKAGAYDFPSPWDVTVP 242
QY 244 EAKNLINOMLTINPAKRITAEALHPWVQCRSTVASMHRQETVBCLKFNARKLKGA 303
Db 243 EAKDLINKMLTINPSKRITAAEALKHPWISHRSTVASOMHRQETVDCCLKFNARKLKGA 302
QY 304 ILTMTLATRNFSVGRQTTPATMTASTAASGTTMGLVEQAKSLNKKADGKVPQTNSTKNSA 363
Db 303 ILTMTLATRNFSGG-----KSGGKNKSDGV-----327
QY 364 AATSPKGLTPAALPQTTVIHNPVDGKESDSANTTIEDAKARKOEIKTTEQLIE 423
Db 328 -----KESSESTNTTIEDTKVKOEIKTTEQLIE 359
QY 424 AVNNGDFEAYA-----FYFENLLAKNSKPIHTTILNPHV 457
Db 360 AINSNGGFESYTKMCDPGMTAFEPALGNLVEGLDFHRFYFENLWSRNSKPVHTTILNPHI 419
QY 458 HVGIEDAACIAYIRLTOYIDGGRPTSQSEETRWHRDQKQWNVHFCSCGAP 511
Db 420 HLMGDESACIAYIRITQYILDAGGIPRTAQSEETRWHRDQKQWIVHFRSGAP 473

```

## RESULT 10

```

KCCA_MOUSE
ID KCCA_MOUSE STANDARD; PRT: 478 AA.
AC P11798; Q61284;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type II alpha chain
DE (EC 2.7.1.123) (CaM-kinase II alpha chain) (CaM kinase II alpha
DE subunit) (CaM-II alpha subunit).
GN CAMK2A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

```



Db 241 VPEAKNLIINOMLTINPAKRITADQALHPWCQKSTVASMRRQTVTECLRKFNARKKL 300  
 QY 301 KGAILTMTLATRNFSVGRQTTAPATMSTRASCTTWGLVEQAKSLANKKAD-GVKPQTNST 359  
 Db 301 KGAILTMTLVSFNESA-----AKSILNKKSDGGVKPQSNN- 335  
 QY 360 KNSAAASPGKTPPAALEPQTVIHNVPDVGKESDSANTTTDEDEKA----- 409  
 Db 336 KNS-----LEPQTVVHNATDGIKGSTCNTTTEDDLKAKSPGSRSD 381  
 QY 410 -----RQEIILKTEQLEIAYVNNDFEAYA----- 434  
 Db 382 KTAPEGNQQPQSLCSSAMRKEIILKTEQLEIAYVNNDFEAYTKICDPGLTSPEPALG 441  
 QY 435 -----FYENLLAKNSKPIHTILNP 455  
 Db 442 NLVEGMDPHKFTFYENLLSKNSKPIHTILNP 472  
 RESULT 12  
 CSCP\_HUMAN  
 ID CSCP\_HUMAN STANDARD; PRT; 926 AA.  
 AC O14936; O43215; Q9NBY3;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Peripheral plasma membrane protein CASK (EC 2.7.1.-) (hCASK)  
 DE (Calcium/calmodulin-dependent serine protein kinase) (Lin-2 homolog).  
 OS CASK OR LIN2.  
 GN Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain, Liver, and Lung;  
 RX MEDLINE=98327121; PubMed=9660868;  
 RA Cohen A.R., Woods D.F., Marfatia S.M., Walther Z., Chishti A.H.,  
 RA Anderson J.M.;  
 RA "Human CASK/LIN-2 binds synectin-2 and protein 4.1 and localizes to  
 RT the basolateral membrane of epithelial cells.";  
 RL J. Cell Biol. 142:129-138(1998).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RA Zha D., Hu G.;  
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
 [3]  
 RP SEQUENCE OF 173-926 FROM N.A.  
 RC TISSUE=fetal;  
 RX MEDLINE=20458875; PubMed=11003712;  
 RA Stevenson D., Lavery H.G., Wenwieser S., Douglas M., Wilson J.B.;  
 RT "Mapping and expression analysis of the human CASK gene.";  
 RL Mamm. Genome 11:934-937(2000).  
 [4]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 489-572..  
 RX MEDLINE=98206299; PubMed=9546224;  
 RA Daniels D.L., Cohen A.R., Anderson J.M., Bruenger A.T.;  
 RT "Crystal structure of the hCASK PDZ domain reveals the structural  
 RT basis of class II PDZ domain target recognition.";  
 RL Nat. Struct. Biol. 5:317-325(1998).  
 CC -!- FUNCTION: BIND TO CELL-SURFACE PROTEINS, INCLUDING AMYLOID  
 CC PRECURSOR PROTEIN, NEURXINS, AND SYNECANS, MAY MEDIATE A LINK  
 CC BETWEEN THE EXTRACELLULAR MATRIX AND THE ACTIN CYTOSKELETON VIA  
 CC ITS INTERACTION WITH SYNECAN AND WITH THE ACTIN/SPECTRIN-BINDING  
 CC PROTEIN 4.1.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (potential).  
 CC -!- TISSUE SPECIFICITY: Ubiquitous.  
 CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE SER/THR  
 CC FAMILY OF PROTEIN KINASES. CASK SUBFAMILY.  
 CC -!- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.  
 CC LIN-27/CASK SUBFAMILY.  
 CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.

CC -!- SIMILARITY: Contains 1 SH3 domain.  
 CC -!- SIMILARITY: Contains 1 guanylate kinase-like domain.  
 CC -----  
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 CC -----  
 CC EMBL: AF032119; AAB88125.1; -  
 CC DR EMBL: AF035982; AAB88198.1; -  
 CC DR EMBL: AF262404; AAF72666.1; -  
 CC DR PDB: IKWA; 27-MAR-98.  
 CC DR PDB: IKWA; 13-FEB-02.  
 CC DR Genew; HGNC:1497; CASK.  
 CC DR MIM; 300172; -  
 CC DR GO; GO:0015629; C:actin cytoskeleton; TAS.  
 CC DR GO; GO:0005886; C:plasma membrane; TAS.  
 CC DR GO; GO:0004384; F:membrane-associated guanylate kinase; TAS.  
 CC DR GO; GO:0007155; P:cell adhesion; TAS.  
 CC DR InterPro; IPR000619; Guanylate\_kin.  
 CC DR InterPro; IPR001472; L27.  
 CC DR InterPro; IPR001478; PDZ.  
 CC DR InterPro; IPR000719; Prot\_kinase.  
 CC DR InterPro; IPR002230; Ser\_thr\_kinase.  
 CC DR InterPro; IPR001452; SH3.  
 CC DR Pfam; PF00018; SH3; 1.  
 CC DR Pfam; PF00069; pkinase; 1.  
 CC DR Pfam; PF00595; PDZ; 1.  
 CC DR Pfam; PF00625; Guanylate\_kin; 1.  
 CC DR Pfam; PF02828; L27; 2.  
 CC DR ProDom; PD000001; Prot\_kinase; 1.  
 CC DR ProDom; PD000066; SH3; 1.  
 CC DR SMART; SM00072; Gukc; 1.  
 CC DR SMART; SM00569; L27; 2.  
 CC DR SMART; SM00228; PDZ; 1.  
 CC DR SMART; SM00220; S\_TKc; 1.  
 CC DR SMART; SM00326; SH3; 1.  
 CC DR SMART; SM00219; TyKc; 1.  
 CC DR PROSITE; PS00856; GUANYLATE\_KINASE\_1; 1.  
 CC DR PROSITE; PS50052; GUANYLATE\_KINASE\_2; 1.  
 CC DR PROSITE; PS50106; PDZ; 1.  
 CC DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 CC DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; FALSE\_NEG.  
 CC DR PROSITE; PS50002; SH3; 1.  
 CC DR Transferrase; Serine/threonine-protein kinase; ATP-binding; SH3 domain;  
 CC Membrane; Calmodulin-binding; 3D-structure.  
 CC DR DOMAIN 12 276 PROTEIN KINASE.  
 CC FT DOMAIN 305 315 CALMODULIN-BINDING.  
 CC FT DOMAIN 489 564 PDZ.  
 CC FT DOMAIN 615 682 SH3.  
 CC FT DOMAIN 739 926 GUANYLATE KINASE.  
 CC FT NP\_BIND 18 26 ATP (BY SIMILARITY).  
 CC FT BINDING 41 41 ATP (BY SIMILARITY).  
 CC FT ACT\_SITE 141 141 BY SIMILARITY.  
 CC FT CONFLICT 340 345 MISSING (IN REF. 2).  
 CC FT CONFLICT 401 401 P -> L (IN REF. 2).  
 CC FT CONFLICT 479 479 G -> D (IN REF. 2).  
 CC FT CONFLICT 580 602 MISSING (IN REF. 2).  
 CC FT CONFLICT 675 675 P -> S (IN REF. 1).  
 CC FT CONFLICT 719 723 MISSING (IN REF. 1).  
 CC FT CONFLICT 780 780 K -> R (IN REF. 1).  
 CC FT STRAND 489 495  
 CC FT STRAND 503 506  
 CC FT HELIX 510 512  
 CC FT STRAND 513 518  
 CC FT TURN 520 521  
 CC FT HELIX 523 527  
 CC FT TURN 528 528  
 CC FT TURN 532 533

FT STRAND 535 539  
 FT TURN 540 541  
 FT STRAND 542 543  
 FT HELIX 544 546  
 FT STRAND 549 558  
 FT STRAND 561 568  
 SQ SEQUENCE 926 AA; 105064 MW; D08D4372B8B60435 CRC64;  
 Query Match 27.1%; Score 736; DB 1; Length 926;  
 Best Local Similarity 35.6%; Pred. No. 1.2e-39;  
 Matches 182; Conservative 88; Mismatches 185; Indels 56; Gaps 11;  
 QY 10 FTDEQLYEDIGKGFSEVRRCKVLCCTGHEVAAKTIINTKK-----LSARDHQLERAR 63  
 DB 8 FDEVTELCEVIGKGFSEVRRCKVLCCTGHEVAAKTIINTKK-----LSARDHQLERAR 64  
 QY 64 ICRLLKHSNIYRLHDSISEEGHYLVFDLVGTGGELEFIVARE-----YYSEADASHCIQQ 119  
 DB 65 ICHMLKHPHIVELLETSYSDGMLYVWFPMGADLCFELVKRADAGFVYSEAVASHYMRQ 124  
 QY 120 ILEAVLHCHQMGVYHRLDKPENLLASKCKGAAYKLADFGLAIEVQDQOQAFGAGTTPG 179  
 DB 125 ILEALRYCHDNNIHRDVKPHCVLLASKENSAPVKLGFGVAILGSGSLVAGGVRGTPH 184  
 QY 180 YLSPEVLRKEAYGKPVDIWACGVILYLLVGYPPWDEDOHKLYQOIKAGAYDFPSPWD 239  
 DB 185 FMAPEVVRKEPYGKPVWCGVILLLSGLCLPYG-TKERLFEGEIKGKYMNPQNS 243  
 QY 240 TVTPEAKNLINQMLTINPAKRITAEHALKHPWVQORSTVASMHRQETVECLKKFNARK 299  
 DB 244 HISESAKDLVRRMLDPAERITVYEAALNHPWLKERDRIYAKIHLPEVTEQLRKFNARK 303  
 QY 300 LKGAILTMTLATRNFVSGRQTTPATMTASTAAGSTTGMVLV-EQAKSLLNKKADGVKPTN 357  
 DB 304 LKGAVALAA-VSSHKENSFYGDPEELPDFSEDPFSGLLAERAVSQVLDSEELHALTD 362  
 QY 358 STKNSA-----AATSPKGTLPAALEPOTTVIHNVPDGIKES 394  
 DB 363 CSEKDLDFLHVSFVDFQHLHTLLDYDKINTKSSPOIRNPPS-----DAVQRAKEV 412  
 QY 395 SDSANTTIEDEDAKARKOEIKTEQLIEAVNNGDFEAYAFYFENLIANKSPITITLN 454  
 DB 413 LEETISCPENNDKELKR--ILTPQHFMAQLQTHDVVAHEVYSDEAL-RVTPPTSPYLN 469  
 QY 455 ---PHVHVGEDACIAYIRLTQYIDQGRP 482  
 DB 470 GDSPEASGMDMENVTRVRLVQFKNTDEP 500  
 RESULT 13  
 ID CSKP\_RAT STANDARD; PRT; 909 AA.  
 AC Q62915;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Peripheral plasma membrane protein CASK (EC 2.7.1.-)  
 DE (Calcium/calmodulin-dependent serine protein kinase).  
 GN CASK.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96256685; PubMed=8786425;  
 RA Hata Y., Butz S., Suedhof T.C.;  
 RT "CASK: a novel dlg/PSD95 homolog with an N-terminal calmodulin-  
 RT dependent protein kinase domain identified by interaction with  
 RT neurexins";  
 RL J. Neurosci. 16:2488-2494(1996).  
 CC -!- FUNCTION: BIND TO CELL-SURFACE PROTEINS, INCLUDING AMYLOID  
 CC PRECURSOR PROTEIN, NEUREXINS, AND SYNDECANS. MAY MEDIATE A LINK



[illegible]

Query Match	26.7%;	Score 725;	DB 1;	Length 924;
Best Local Similarity	34.6%;	Pred. NO. 5.9e-39;		
Matches 179: Conservative	90;	Mismatches 180;	Indels 158;	Gap 13

Qy	10	F7DEYQLYVEDIGKGAFSVVRR	CVKLCCTGHEYAAKIINTKK-----LSARHQKLEAREAR	63
Db	8	FEDVYELCEVIGKPSVVRR	CINRRINRGQQQFAVKTVDAKFTSGPLSTED---LKREAS	64
Qy	64	ICRLKHSNIVRLHDSISEGFFHYLV	FDLVTGGEIFEDIVARE---YYSEADASHCICQ	119
Db	65	ICMLKHPIHVELLEYYSDDGMLTW	VEFFDGADLCPIVKRDAGFVYSEAVASHTRQ	124
Qy	120	ILEAVLHCHQGVVHRDLKPNELLAS	CKGGAVKLADFGLAIEVGQDQAWFGAGTGP	179
Db	125	ILEALRYCHDNIIHRRVPHCVLLAS	KENSAPVVLGGFGVAIQLGESIVAGRGVGTPI	184
Qy	180	YLSPEVLKRAYKQVDDIWACQVIT	YLLVGPYEPWDEDHQLYQQIQAGAYDPSPEWD	239
Db	185	FWAPEVWRREYKQVDDWGGCVIL	FILLSCGLPYFG--TKERLFEGILKGYKKNPQWS	243
Qy	240	TYTPEAKNLINQMILTINPAKRIT	AHEKHPWVQOORTVASMMHROETVECKLFENARRK	299
Db	244	HISEGAKDLVRMLMLDPAERTTY	TEALNHPMLKPERDAYKHLPEFTVEQIURLNARRK	303

300 LKGAILLTMTLATRNFSVSGQTTPATATWTAASGTTMGLV--EQAKSLNKKADGVKQQTIN 357  
 304 LKGAIVLAA-VSSHKFNSFYGDPPFELPDSFTSSGLLAARFAVSQVLDSLEIHALTD 362  
 358 STPKNSA-----AATSPKGLTPPAALPEQTTVIHNPVDGIKES 394  
 363 CSERDLDFLHSVQDQHLHTLFDLYDKINTKSSFOINRPPS-----DAVQRAKEV 412  
 395 SSDSANTTIEDAKAKQEIITKTQLLIEAVNNGDFFAVTFENILAKNSKPIHTTILN 454  
 413 LREITSCEYPENNDAKELKR--ILTQPHFWALLQTHDVVAHEVYSDGALRVTPPP-----TS 465  
 455 PHVHVHIG-----DAACIATVIRLFOYIDGQGRP 482  
 466 PVLN--GDSFESANGDMDMENTVRLVQFOKNTDEP 500

RESULT 15  
 KCCA RAT  
 ID KCC4\_RAT STANDARD; PRT; 474 AA.  
 AC PC1234;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-APR-1993 (Rel. 42, Last sequence update)  
 DT 13-SEP-2003 (Rel. 42, Last annotation update)  
 DE Calcium/calmodulin-dependent protein kinase type IV catalytic chain  
 DE (CaC 2.7.1.123) (CAM kinase-GR) (CAMK IV) (Calipermin).  
 GN CAMK4.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND PARTIAL SEQUENCE.  
 RX MEDLINE=91288548; PubMed=1648230;  
 RA Ostmiede C.-A., Bland M.M., Merrill B.M., Sahyoun N.;  
 FT "Relationship of genes encoding Ca2+/calmodulin-dependent protein  
 FT kinase Gr and calpermin: a gene within a gene.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:5784-5788(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RX MEDLINE=91304387; PubMed=1649385;  
 RA Means A.R., Cruzalegui F., Lemagueresse B., Needleman D.S.,  
 RA Slaughter G.R., Ono T.;  
 FT "A novel Ca2+/calmodulin-dependent protein kinase and a male germ  
 FT cell-specific calmodulin-binding protein are derived from the same  
 FT gene.";  
 RL Mol. Cell. Biol. 11:3960-3971(1991).  
 RN [3]  
 RP SEQUENCE OF 250-474 FROM N.A. (ISOFORM 1).  
 RX STRAIN=Sprague-Dawley;  
 RX MEDLINE=89174647; PubMed=2538431;  
 RA Ostmiede C.-A., Jensen K.F., Sahyoun N.;  
 FT "Ca2+/calmodulin-dependent protein kinase enriched in cerebellar  
 FT granule cells. Identification of a novel neuronal  
 FT calmodulin-dependent protein kinase.";  
 RL J. Biol. Chem. 264:5866-5875(1989).  
 RN [4]  
 RP SEQUENCE OF 306-474 FROM N.A. (ISOFORM 2), AND SEQUENCE OF 335-361.  
 RX STRAIN=Sprague-Dawley;  
 RX MEDLINE=89123372; PubMed=2914893;  
 RA Ono T., Slaughter G.R., Cook R.G., Means A.R.;  
 FT "Molecular cloning sequence and distribution of rat calpermin, a  
 FT high affinity calmodulin-binding protein.";  
 RL J. Biol. Chem. 264:2081-2087(1989).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RX MEDLINE=96094352; PubMed=7493991;  
 RA Sun Z., Means R.L., Lemagueresse B., Means A.R.;  
 FT "Organization and analysis of the complete rat calmodulin-dependent  
 FT protein kinase IV gene.";  
 RL J. Biol. Chem. 270:29507-29514(1995).  
 RN [6]  
 RP -1- FUNCTION: CAM KINASE GR IS A NEURONAL-SPECIFIC PROTEIN KINASE,

[illegible]

Search completed: October 10, 2003, 08:08:33  
Job time : 25 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: October 10, 2003, 07:48:21 ; Search time 114 Seconds  
(without alignments)  
1168.028 Million cell updates/sec

Title: US-09-820-790B-2  
Perfect score: 2715  
Sequence: 1 MATVTCTRTDEYQLYEDI.....DGKWNVHCGGAPVAPLQ 516

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_virus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Description
1	2663	98.1	Q8b141 mus musculus
2	2571	94.7	Q93560 gallus galli
3	2526	93.0	Q91549 xenopus lae
4	2441.5	89.9	Q91587 xenopus lae
5	2374.5	87.5	Q63094 rattus norv
6	2286.5	84.2	Q95265 mustela put
7	2256	83.1	Q9d900 xenopus lae
8	2248.5	82.8	Q8n413 homo sapien
9	2243	82.6	Q8n413
10	2230	82.1	Q8n413
11	2225.5	82.0	Q95262 mustela put
12	2223	81.9	Q9dfz8 xenopus lae
13	2214.5	81.6	Q9d901
14	2204	81.2	Q8cac5 mus musculus
15	2186.5	80.5	Q95263 mustela put
16	2170	79.9	Q9dfz9 xenopus lae

17	2146	79.0	566	4	Q8NIA4
18	2134.5	78.6	487	6	Q8NMW7
19	2077	76.5	478	4	Q8N553
20	2077	76.5	499	6	Q95266
21	2076	76.5	478	11	Q9CZE2
22	2062	75.9	499	6	Q77708
23	2043	75.2	475	13	Q9DG02
24	2015.5	74.2	527	4	Q9I2H4
25	2011.5	74.1	478	4	Q8IWE0
26	1997.5	73.6	450	6	Q77706
27	1993	73.4	489	13	Q93559
28	1984.5	73.1	478	13	Q9YHB8
29	1941	71.5	456	4	Q8WU40
30	1886	69.5	561	6	Q8NMW5
31	1865	68.7	509	5	Q9V495
32	1854.5	68.3	530	5	Q00168
33	1638	60.3	482	5	Q9U6Q0
34	1630.5	60.1	559	5	Q21431
35	1629	60.0	518	5	Q9NH57
36	1628	60.0	520	5	Q9NH60
37	1618.5	59.6	533	5	Q9NH59
38	1613	59.4	361	11	Q8CCM0
39	1602.5	59.0	571	5	Q9NH58
40	1592	58.6	361	11	Q8BVG2
41	1541	56.8	720	5	Q62305
42	1488	54.8	360	5	Q94609
43	1477	54.4	360	5	Q94608
44	1403.5	51.7	306	4	Q00561
45	1368	50.4	350	5	Q9NG91

## ALIGNMENTS

RESULT 1

Q8BL41	PRELIMINARY;	PRT;	542 AA.
ID	Q8BL41		
AC	Q8BL41		
DT	01-MAR-2003 (TRENBLrel. 23, Created)		
DT	01-MAR-2003 (TRENBLrel. 23, Last sequence update)		
DE	Calcium/calmodulin-dependent protein kinase type II beta chain.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Brain;		
RX	MEDLINE=22354683; PubMed=12466851;		
RA	The FANTOM Consortium,		
RA	the KIKEN Genome Exploration Research Group Phase I & II Team;		
RT	*Analysis of the mouse transcriptome based on functional annotation of		
RT	60,770 full-length cDNAs.*;		
RL	Nature 420:563-573(2002).		
DR	EMBL: AK046454; BAC32736.1;		
SQ	SEQUENCE 542 AA; 60495 MW; 454FFB0D89C7925A CRC64;		

Query Match 98.1%; Score 2663; DB 11; Length 542;  
Best Local Similarity 93.9%; Pred. No. 2.3e-204;  
Matches 509; Conservative 3; Mismatches 4; Indels 26; Gaps 1;

QY	1	MATVTCTRTDEYQLYEDI	IGKGF	SVVRCVKLC	TGHE	YAAKI	INTKLS	ARDHOK	LER 60
Db	1	MATVTCTRTDEYHL	YED	IGKGF	SVVRCVKLC	TGHE	YAAKI	INTKLS	ARDHOK
QY	61	EARTCLLKHSNIVRLHDS	ISIE	EGFHYLV	FDLY	TG	GE	FDIV	AREY
Db	61	EARTCLLKHSNIVRLHDS	ISIE	EGFHYLV	FDLY	TG	GE	FDIV	AREY
QY	121	LEAVLHCHQGVVHRDL	KPEN	LLAS	KCKGA	AVK	LAD	FG	LA
Db	121	LEAVLHCHQGVVHRDL	KPEN	LLAS	KCKGA	AVK	LAD	FG	LA



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QY 181 LSPVLRKEAYGKPDVWAGGVILYLLVGYPPFWEDEQHKLYQKAGAYDPPSPENDT 240
DB 181 LSPVLRKEAYGKPDVWAGGVILYLLVGYPPFWEDEQHKLYQKAGAYDPPSPENDT 240
QY 241 VTPEAKNLINQMLTINPAKRITAHEALKHPWCQSRSTVASMHRQETVECLKFNARRKL 300
DB 241 VTPEAKNLINQMLTINPAKRITAHEALKHPWCQSRSTVASMHRQETVECLKFNARRKL 300
QY 301 KGALLTMTLATRNFVSGRQTAPATMTAAAGTTMGLVEQAKSLNKKADGVKPTQNSTK 360
DB 301 KGALLTMTLATRNFVSGRQTAPATMTAAAGTTMGLVEQAKSLNKKADGVKPTQNSTK 360
QY 361 NSAAATSPKGTLPPLAALPQTTVHNPDVGIKESDSSANTTIEDAKARKQEIILKTTEQ 420
DB 361 NSAAATSPKGTLPPLAALPQTTVHNPDVGIKESDSSANTTIEDAKARKQEIILKTTEQ 420
QY 421 LIEAVNNGDFEAYA-----FYFENLLAKSKPIHTTILN 454
DB 421 LIEAVNNGDFEAYA-----FYFENLLAKSKPIHTTILN 454
QY 455 PHVHVIGEDAACIAYIRLTQYIDQGRPTQSESETRVWHRDCKWONVHFHCGAPVAP 514
DB 455 PHVHVIGEDAACIAYIRLTQYIDQGRPTQSESETRVWHRDCKWONVHFHCGAPVAP 514
QY 481 PHVHVIGEDAACIAYIRLTQYIDQGRPTQSESETRVWHRDCKWONVHFHCGAPVAP 540
DB 481 PHVHVIGEDAACIAYIRLTQYIDQGRPTQSESETRVWHRDCKWONVHFHCGAPVAP 540
QY 515 LQ 516
DB 515 LQ 516
QY 541 LQ 542
DB 541 LQ 542

RESULT 2
O93560 PRELIMINARY; PRT; 540 AA.
AC O93560;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Calcium/calmodulin-dependent kinase type II beta subunit.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-bred White Leghorn; TISSUE-Forebrain;
RA Li G.Y., Cooper N.G.F.;
RT "Molecular cloning and analysis of calcium/calmodulin-dependent
RT protein kinase II from chicken brain.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DDAJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF065249; AAC79460.1; -.
DR HSSP; O63450; IA06.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 540 AA; 60180 MW; DA5F4D3A8E9DF2E CRC64;

Query Match 94.7%; Score 2571; DB 13; Length 540;
Best Local Similarity 90.8%; Pred. No. 5.3e-197;
Matches 492; Conservative 9; Mismatches 13; Indels 28; Gaps 2;

QY 1 MATTVTCRTFTDEYQLYEDIGKGAFSVVRCVKLTGHEYAAKINTKKLSARDHOKLER 60
DB 1 MATTVTCRTFTDEYQLYEDIGKGAFSVVRCVKLTGHEYAAKINTKKLSARDHOKLER 60
QY 61 EARICRLLKHSNIVRLHDSISEEGFHYLVFDLTGSELFDVLVAREYISEADASHCIQOI 120

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DB 61 EARICRLLKHSNIVRLHDSISEEGFHYLVFDLTGSELFDVLVAREYISEADASHCIQOI 120
QY 121 LEAVLHCHQMGVVRHDLKPNELLASKCKGAAYKLAIDFGLAIEVQDQQAQWFGFAGTPEY 180
DB 121 LEAVLHCHQMGVVRHDLKPNELLASKCKGAAYKLAIDFGLAIEVQDQQAQWFGFAGTPEY 180
QY 181 LSPVLRKEAYGKPDVWAGGVILYLLVGYPPFWEDEQHKLYQKAGAYDPPSPENDT 240
DB 181 LSPVLRKEAYGKPDVWAGGVILYLLVGYPPFWEDEQHKLYQKAGAYDPPSPENDT 240
QY 241 VTPEAKNLINQMLTINPAKRITAHEALKHPWCQSRSTVASMHRQETVECLKFNARRKL 300
DB 241 VTPEAKNLINQMLTINPAKRITAHEALKHPWCQSRSTVASMHRQETVECLKFNARRKL 300
QY 301 KGALLTMTLATRNFVSGRQTAPATMTAAAGTTMGLVEQAKSLNKKADGVKPTQNSTK 360
DB 301 KGALLTMTLATRNFVSGRQTAPATMTAAAGTTMGLVEQAKSLNKKADGVKPTQNSTK 360
QY 361 NSAAATSPKGTLPPLAALPQTTVHNPDVGIKESDSSANTTIEDAKARKQEIILKTTEQ 420
DB 361 NSAAATSPKGTLPPLAALPQTTVHNPDVGIKESDSSANTTIEDAKARKQEIILKTTEQ 420
QY 359 GSAGVTSPKGTLPPLAALPQTTVHNPDVGIKESDSSANTTIEDAKARKQEIILKTTEQ 418
DB 359 GSAGVTSPKGTLPPLAALPQTTVHNPDVGIKESDSSANTTIEDAKARKQEIILKTTEQ 418
QY 421 LIEAVNNGDFEAYA-----FYFENLLAKSKPIHTTILN 454
DB 421 LIEAVNNGDFEAYA-----FYFENLLAKSKPIHTTILN 454
QY 419 LIEAVNNGDFEAYA-----FYFENLLAKSKPIHTTILN 478
DB 419 LIEAVNNGDFEAYA-----FYFENLLAKSKPIHTTILN 478
QY 455 PHVHVIGEDAACIAYIRLTQYIDQGRPTQSESETRVWHRDCKWONVHFHCGAPVAP 514
DB 455 PHVHVIGEDAACIAYIRLTQYIDQGRPTQSESETRVWHRDCKWONVHFHCGAPVAP 514
QY 479 PHVHVIGEDAACIAYIRLTQYIDQGRPTQSESETRVWHRDCKWONVHFHCGAPVAP 538
DB 479 PHVHVIGEDAACIAYIRLTQYIDQGRPTQSESETRVWHRDCKWONVHFHCGAPVAP 538
QY 515 LQ 516
DB 515 LQ 516
QY 539 LQ 540
DB 539 LQ 540

RESULT 3
Q91549 PRELIMINARY; PRT; 540 AA.
AC Q91549;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Calmodulin dependent protein kinase II beta subunit.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RA Taylor W.L.;
RT "NONE.";
RL Submitted (FEB-1994) to the EMBL/GenBank/DDAJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U06636; AAB81938.1; -.
DR HSSP; O63450; IA06.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 540 AA; 60480 MW; 199F8DC86FDB456D CRC64;

Query Match 93.0%; Score 2526; DB 13; Length 540;
Best Local Similarity 89.4%; Pred. No. 2.1e-193;
Matches 481; Conservative 14; Mismatches 17; Indels 26; Gaps 1;

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QY 5 VTCRFTDEYQVLEDIGKAFSVVRCVKLCTGHEHYAAKIINTKLSARDHQKLERARI 64  
 DB 3 VTCRFTDEYQVLEEGKAFSVVRCVKLCTGHEHYAAKIINTKLSARDHQKLERARI 62  
 QY 65 CRLLKHSNIVRLHDSISSEGFHYLFDLVTGGELFEDIVAREYVSEADASHCIIQILEAV 124  
 DB 63 CRLLKHPNIVRLHDSISSEGFHYLFDLVTGGELFEDIVAREYVSEADASHCIIQILEAV 122  
 QY 125 LHCQMGVYVHRDLKPNLLASCKCKGAAYKLADFGLAIEVQDQQAQWFGAGTGGYLSPE 184  
 DB 123 LHCQMGVYVHRDLKPNLLASCKCKGAAYKLADFGLAIEVQDQQAQWFGAGTGGYLSPE 182  
 QY 185 VLKREAYGKPVDIWAGGVILYLLVGYPPFWDEQDKLYQOIKAGAYDPPSPWDVTYPE 244  
 DB 183 VLKREAYGKPVDIWAGGVILYLLVGYPPFWDEQDKLYQOIKAGAYDPPSPWDVTYPE 242  
 QY 245 AKNLINQMLTINPAKRITAEALAKHPWVCQSTVASMHRQETVECLKFNARKKLKGA 304  
 DB 243 AKNLINQMLTINPAKRITAEALAKHPWVCQSTVASMHRQETVECLKFNARKKLKGA 302  
 QY 305 LTTMLATRNFSVGRQTAPATMSTAAGTNGLVQAKSLINKKADGVKPKQTNSTKNSAA 364  
 DB 303 LTTMLATRNFSVGRQTAPATMSTAAGTNGLVQAKSLINKKADGVKPKQTNSTKNSAG 362  
 QY 365 ATSPKGTLPAALEPQTTVIHNPVDGKESDSANTTIEDDAKARKOEIKITTEOLIEA 424  
 DB 363 VTSKPGPIPPAAL-ESDSTHNPDEEEMKARKOEIKITTEOLIEA 422  
 QY 425 VNNGDFEAYA-----FYFENLLAKSNKPIHTTILNPHVH 458  
 DB 423 VNNGDFEAYAKICDPLGTTTPEALGNLVEGIDFHRFYFENLLSKNKPHTTILNPHVH 482  
 QY 459 VIGDEACIAIYRLTOYIDQGRPTQSSETRVWHRDQKQWNVHFCSGAPVAPLQ 516  
 DB 483 VIGDEACIAIYRLTOYIDQGRPTQSSETRVWHRDQKQWNVHFCSGAPVAPLQ 540

RESULT 4

Q91587 ID Q91587 PRELIMINARY; PRT; 525 AA.  
 AC Q91587  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, last annotation update)  
 DE Calcium/calmodulin-dependent kinase type II beta'-subunit.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kanki H., Poo M.;  
 RT "Cloning and functional analysis of Xenopus laevis Calcium/calmodulin-  
 dependent kinase type II beta'-subunit."  
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
 CC -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; U18196; AAA57338.1; -;  
 DR HSP; Q63450; 1A06.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00101; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 525 AA; 58860 MW; 39C915FA4EB7B3B5 CRC64;

Query Match

Best Local Similarity 89.9%; Score 2441.5; DB 13; Length 525;  
 Matches 467; Conservative 14; Mismatches 16; Indels 41; Gaps 2;

QY 5 VTCRFTDEYQVLEDIGKAFSVVRCVKLCTGHEHYAAKIINTKLSARDHQKLERARI 64  
 DB 3 VTCRFTDEYQVLEEGKAFSVVRCVKLCTGHEHYAAKIINTKLSARDHQKLERARI 62  
 QY 65 CRLLKHSNIVRLHDSISSEGFHYLFDLVTGGELFEDIVAREYVSEADASHCIIQILEAV 124  
 DB 63 CRLLKHPNIVRLHDSISSEGFHYLFDLVTGGELFEDIVAREYVSEADASHCIIQILEAV 122  
 QY 125 LHCQMGVYVHRDLKPNLLASCKCKGAAYKLADFGLAIEVQDQQAQWFGAGTGGYLSPE 184  
 DB 123 LHCQMGVYVHRDLKPNLLASCKCKGAAYKLADFGLAIEVQDQQAQWFGAGTGGYLSPE 182  
 QY 185 VLKREAYGKPVDIWAGGVILYLLVGYPPFWDEQDKLYQOIKAGAYDPPSPWDVTYPE 244  
 DB 183 VLKREAYGKPVDIWAGGVILYLLVGYPPFWDEQDKLYQOIKAGAYDPPSPWDVTYPE 242  
 QY 245 AKNLINQMLTINPAKRITAEALAKHPWVCQSTVASMHRQETVECLKFNARKKLKGA 304  
 DB 243 AKNLINQMLTINPAKRITAEALAKHPWVCQSTVASMHRQETVECLKFNARKKLKGA 302  
 QY 305 LTTMLATRNFSVGRQTAPATMSTAAGTNGLVQAKSLINKKADGVKPKQTNSTKNSAA 364  
 DB 303 LTTMLATRNFSVGRQTAPATMSTAAGTNGLVQAKSLINKKADGVKPKQTNSTKNSAG 362  
 QY 365 ATSPKGTLPAALEPQTTVIHNPVDGKESDSANTTIEDDAKARKOEIKITTEOLIEA 424  
 DB 363 VTSKPGPIPPAAL-ESDSTHNPDEEEMKARKOEIKITTEOLIEA 407  
 QY 425 VNNGDFEAYA-----FYFENLLAKSNKPIHTTILNPHVH 458  
 DB 408 VNNGDFEAYAKICDPLGTTTPEALGNLVEGIDFHRFYFENLLSKNKPHTTILNPHVH 467  
 QY 459 VIGDEACIAIYRLTOYIDQGRPTQSSETRVWHRDQKQWNVHFCSGAPVAPLQ 516  
 DB 468 VIGDEACIAIYRLTOYIDQGRPTQSSETRVWHRDQKQWNVHFCSGAPVAPLQ 525

RESULT 5

Q63094 ID Q63094 PRELIMINARY; PRT; 589 AA.  
 AC Q63094;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, last annotation update)  
 DE Calcium/calmodulin-dependent protein kinase II, beta 3 isoform.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=Pancratic islets;  
 RX MEDLINE=95121451; PubMed=7821422;  
 RA Urquidí V., Ashcroft S.J.H.;  
 RT "A novel pancreatic beta-cell isoform of calcium/calmodulin-dependent  
 protein kinase II (beta 3 isoform) contains a proline-rich tandem  
 repeat in the association domain."  
 RL FEBS Lett. 358:23-26(1995).  
 CC -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; X83375; CAA58289.1; -;  
 DR HSP; Q63450; 1A06.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00101; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 589 AA; 64976 MW; C108DE09A1ACC4CB CRC64;

Query Match 87.5%; Score 2374.5; DB 11; Length 589;  
Best Local Similarity 75.0%; Pred. No. 3.2e-181;  
Matches 471; Conservative 2; Mismatches 4; Indels 151; Gaps 4;

QY 1 MATVTCTRTDEYQYEDIGKGFASVVRRCVKLCGTGHEYAAKIINTKLSARDHQKLER 60  
|||||  
Db 1 MATVTCTRTDEYQYEDIGKGFASVVRRCVKLCGTGHEYAAKIINTKLSARDHQKLER 60  
|||||

QY 61 EARICLLKHSNIVRLHDSISEEGFHYLVDFDLVTGGELFEDIVAREYSEADASHCIQOI 120  
|||||  
Db 61 EARICLLKHSNIVRLHDSISEEGFHYLVDFDLVTGGELFEDIVAREYSEADASHCIQOI 120  
|||||

QY 121 LEAVLHCHQMVVHRDLKPEINLLASKCKGAAYKVLADFGLEAVGQDQQAQWFGAGTPTGY 180  
|||||  
Db 121 LEAVLHCHQMVVHRDLKPEINLLASKCKGAAYKVLADFGLEAVGQDQQAQWFGAGTPTGY 180  
|||||

QY 181 LSPVLKREAYGKPYDINACGVILYLLVGYPPFWDEDOHKLYQOIKAGAYDPPSPEDWT 240  
|||||  
Db 181 LSPVLKREAYGKPYDINACGVILYLLVGYPPFWDEDOHKLYQOIKAGAYDPPSPEDWT 240  
|||||

QY 241 VTPEAKNLINQMLTINPAKRITAEALKHPWCORSTVASMMHROETVECLKFNARRKL 300  
|||||  
Db 241 VTPEAKNLINQMLTINPAKRITAEALKHPWCORSTVASMMHROETVECLKFNARRKL 300  
|||||

QY 301 KGAILTMTLATRNFSVGRQTTAPATMTAAAGTTNGLVQOAKSLNKKADGVKPTQNSTK 360  
|||||  
Db 301 KGAILTMTLATRNFS- - - - - AKSLNKKADGVKPTQNSTK 336  
|||||

QY 361 NSAAATSPKGTLPAALEPQTTVHNPDVGKESDSANTTIEDAKA- - - - - 409  
|||||  
Db 337 NSSALTSPKSLPAAAL- - - - - ESSDSTNTTIEDAKAPRISDIILNSVR 381  
|||||

QY 410 - - - - - 409

Db 382 RCGCTPBAEGFLSVGPPCLSPGLIGLPTSPRISDIILNSVRSGSPPEAGLPPVGGP 441  
|||||

QY 410 - - - - - RKQELIKTTEOLTEAVNNGDFEAYA- - - - - 434  
|||||

Db 442 PCPSETPLGFLPTPSRKQILIKTTEOLTEAVNNGDFEAYAKICDPGLTSFEPBALGNLVE 501  
|||||

QY 435 - - - - - FYFENLLAKNSKPIHTTILNPHVHVGIGEDAACTAYIRLQYIDGQGRPTSQSE 488  
|||||

Db 502 GMDPFRFYFENLLAKNSKPIHTTILNPHVHVGIGEDAACTAYIRLQYIDGQGRPTSQSE 561  
|||||

QY 489 ETRVWHRDCKWQNVHFHCSGAPVAPLQ 516  
|||||  
Db 562 ETRVWHRDCKWQNVHFHCSGAPVAPLQ 589  
|||||

RESULT 6  
Q95265 ID Q95265 PRELIMINARY; PRT; 539 AA.  
AC Q95265;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Cam kinase II gamma G-1 (Calcium/calmodulin-dependent protein kinase  
DE II isoform gamma-G).  
OS Mustela putorius furo (Ferret), and  
OS Sus scrofa (pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;  
OC Mustela.  
OX NCBI\_TaxID=9669, 9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES=M. putorius furo;  
RA Gangopadhyay S.S., Morgan K.G.;  
RT \*Cam Kinase II Gamma Isoforms of Ferret.\*;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC SPECIES=Pig; TISSUE=Aortic smooth muscle;

RX MEDLINE=97238879; PubMed=9083077;  
RA Singer H.A., Benschoter H.A., Schworer C.M.;  
RT "Novel Ca2+/calmodulin-dependent protein kinase II gamma-subunit  
RT variants expressed in vascular smooth muscle, brain, and  
RT cardiomyocytes.";  
RL J. Biol. Chem. 272:9393-9400(1997).  
CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR EMBL; AF464186; AAL69957.1; -  
DR HSP; U72973; AAC48714.1; -  
DR HSP; Q63450; IAO6.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR002290; Ser\_thr\_kinase.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TKc; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 539 AA; 60201 MW; 24989285F7564529 CRC64;

Query Match 84.2%; Score 2286.5; DB 6; Length 539;  
Best Local Similarity 80.8%; Pred. No. 3.1e-174;  
Matches 439; Conservative 32; Mismatches 41; Indels 31; Gaps 4;

QY 1 MATVTCTRTDEYQYEDIGKGFASVVRRCVKLCGTGHEYAAKIINTKLSARDHQKLER 60  
|||||  
Db 1 MATTACTCTRTDDYQLFEELGKGFASVVRRCVKLTQTYAAKIINTKLSARDHQKLER 60  
|||||

QY 61 EARICLLKHSNIVRLHDSISEEGFHYLVDFDLVTGGELFEDIVAREYSEADASHCIQOI 120  
|||||  
Db 61 EARICLLKHSNIVRLHDSISEEGFHYLVDFDLVTGGELFEDIVAREYSEADASHCIQOI 120  
|||||

QY 121 LEAVLHCHQMVVHRDLKPEINLLASKCKGAAYKVLADFGLEAVGQDQQAQWFGAGTPTGY 180  
|||||  
Db 121 LESVNIHQHDIHEDLKPENLLASKCKGAAYKVLADFGLEAVGQDQQAQWFGAGTPTGY 180  
|||||

QY 181 LSPVLKREAYGKPYDINACGVILYLLVGYPPFWDEDOHKLYQOIKAGAYDPPSPEDWT 240  
|||||  
Db 181 LSPVLKREAYGKPYDINACGVILYLLVGYPPFWDEDOHKLYQOIKAGAYDPPSPEDWT 240  
|||||

QY 241 VTPEAKNLINQMLTINPAKRITAEALKHPWCORSTVASMMHROETVECLKFNARRKL 300  
|||||  
Db 241 VTPEAKNLINQMLTINPAKRITADQALKHPWCORSTVASMMHROETVECLKFNARRKL 300  
|||||

QY 301 KGAILTMTLATRNFSVGRQTTAPATMTAAAGTTNGLVQOAKSLNKKAD-GVKPTQNST 359  
|||||  
Db 301 KGAILTMTLVSENFSGVGRQSSAPASPAAGIA- - - GQAKSLNKKSDGGVKPQSN- 356  
|||||

QY 360 KNSAAATSPKGTLPAALEPQTTVHNPDVGKESDSANTTIEDAKAROEIKTTE 419  
|||||  
Db 357 KNSLVSPAEPAPLOTAMEPQTTVINATDGIKSTESCNTTIEDLKVQKEIKTTE 416  
|||||

QY 420 OLIEAVNNGDFEAYA- - - - - FYFENLLAKNSKPIHTTIL 453  
|||||  
Db 417 QLIEAINNGDFEAYTKICDPGLTSFEPBALGNLVBGMDFHFKFYFENLLSKNSKPIHTTIL 476  
|||||

QY 454 NPVHVHVGIGEDAACTAYIRLQYIDGQGRPTSQSEETVWHRDCKWQNVHFHCSGAPVA 513  
|||||  
Db 477 NPVHVHVGIGEDAACTAYIRLQYIDGQGRPTSQSEETVWHRDCKWQNVHFHCSGAPAA 536  
|||||

QY 514 PLQ 516  
|||  
Db 537 PLQ 539

RESULT 7  
Q95265 ID Q95265 PRELIMINARY; PRT; 564 AA.  
AC Q95265;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

Q8N4I3	PRELIMINARY;	PRT;	527 AA.
ID	Q8N4I3		
AC	Q8N4I3;		
DT	01-OCT-2002 (TrEMBLrel. 22, Created)		
DT	01-OCT-2003 (TrEMBLrel. 22, Last sequence update)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)		
DE	Calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma.		
DE	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
OX	[1]		
RN	SEQUENCE FROM N.A.		
RP	TISSUE=Brain;		
RC	Strausberg R.;		
RA	Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.		
RL	EMBL; BC034044; AAH34044.1; -		
DR	InterPro; IPR000719; Prot_kinase.		
DR	InterPro; IPR002290; Ser_thr_kinase.		
DR	InterPro; IPR001245; Tyr_kinase.		
DR	Pfam; PF00069; pkinase; 1.		
DR	ProDom; PD000001; Prot_kinase; 1.		
DR	SMART; SM00220; S_TKc; 1.		
DR	SMART; SM00219; TyrKc; 1.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.		
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.		
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.		
KW	ATP-binding; Kinase; Transferase.		
SK	SEQUENCE 527 AA; 59048 MW; 2C49B8931B364F1A CRC64;		
Query Match 82.8%; Score 2248.5; DB 4; Length 527;			
Best Local Similarity 79.7%; Pred. No. 3.2e-171;			
Matches 433; Conservative 29; Mismatches 38; Indels 43; Gaps 4			
QY	1 MATVTCTRTDQYLYEDIKGAFSVVRCVKLCITGCHYEYAAKINIKKLSARDHOKLER	60	
DB	:     :     :     :     :     :     :     :     :     :		
QY	1 MATTATCTRTDDYQLFEELKGAFSVVRCVKKKTQEYAAKINIKKLSARDHOKLER	60	
DB	:     :     :     :     :     :     :     :     :		
QY	61 EARTCLLKHSNIVRLHDSISEGFLHYLFDLVGTGELFEDIVAREYYSADASHCICQI	120	
DB	:     :     :     :     :     :     :     :     :		
QY	61 EARTCLLKHPNIVRLHDSISEGFLHYLFDLVGTGELFEDIVAREYYSADASHCICHI	120	
DB	:     :     :     :     :     :     :     :     :		
QY	121 LEAVLHCHQGVVHRLDKPENLLASKCKGAAYKLADFGLAIEVGQDQAAWFGAGTPGY	180	
DB	:     :     :     :     :     :     :     :     :		
QY	121 LESYNHITHQHDIVHRLDKPENLLASKCKGAAYKLADFGLAIEVGQDQAAWFGAGTPGY	180	
DB	:     :     :     :     :     :     :     :     :		
QY	181 LSPVELKRAYKFPVDINACGVILYLLVGYFPFWDQHKLYQIQIKAGAYDFPSPWD	240	
DB	:     :     :     :     :     :     :     :     :		
QY	181 LSPVELRKDPYKFPVDINACGVILYLLVGYFPFWDQHKLYQIQIKAGAYDFPSPWD	240	
DB	:     :     :     :     :     :     :     :     :		
QY	241 VTPEAKNLINQMLTINPAKRITAEALHKHPWCQSTVASMHRQETVECLKFNARKKL	300	
DB	:     :     :     :     :     :     :     :     :		
QY	241 VTPEAKNLINQMLTINPAKRITADQALKHPWCQSTVASMHRQETVECLKFNARKKL	300	
DB	:     :     :     :     :     :     :     :     :		
QY	301 KGALITTLMLATRNFSYGRGTAPATMTAASTGTMGLVEQAQKSLNKKAD-GYKPTQNST	359	
DB	:     :     :     :     :     :     :     :     :		
QY	301 KGALITTLMLYSRNFSGVSGSAPASAAGLA---GQAQKSLNKKSDGGVKKRKS	357	
DB	:     :     :     :     :     :     :     :     :		
QY	360 KNSAAATSPKGTLPAALEPQTVIHNPVDCIKESDSSANTTIEDAKAKKEIKTTE	419	
DB	:     :     :     :     :     :     :     :     :		
QY	358 S-----VHLMPQTVVHNATDGIKGTESCNTTDEDLKVKEIHKITE	404	
DB	:     :     :     :     :     :     :     :     :		
QY	420 QLEAVNGDPEAVA-----PYFENLLAKNSKPIHTTIL	453	
DB	:     :     :     :     :     :     :     :     :		
QY	405 QLEIAINNGDPEAYTKICDPLGTSFEPEALGNLVEGMDPHKFFYNLLSKNSKPIHTTIL	464	
DB	:     :     :     :     :     :     :     :     :		
QY	454 NPHVIVIGEDAAACIAIIRLTQYIDGQRPTSSQSEETRVVHRRDCKWNVHFCSGAPYA	513	
DB	:     :     :     :     :     :     :     :     :		
QY	465 NPHVIVIGEDAAACIAIIRLTQYIDGQRPTSSQSEETRVVHRRDCKWNVHFCSGAPYA	524	
DB	:     :     :     :     :     :     :     :     :		
QY	514 PLQ 516		
DB			

Db 525 PLO 527

## RESULTS

```

Q8WNW6 PRELIMINARY; PRT; 516 AA.
ID Q8WNW6
AC Q8WNW6;
DT 01-VAR-2002 (TremBurel. 20, Created)
DT 01-VAR-2002 (TremBurel. 20, Last sequence update)
DT 01-VAR-2003 (TremBurel. 23, Last annotation update)
CaM kinase II gamma H.
DE Mus musculus putorius furo (Ferret).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OC NCBI_TaxID=9669;
RN [1]
SEQUENCE FROM N.A.
RA Gangopadhyay S.S., Morgan K.G.;
RP "CaM Kinase II Gamma Isoforms of Ferret.";
RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF461485; AAL69556.1; -.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR003290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ
SEQUENCE 516 AA; 57796 MW; 141109E5974457AF CRC64;

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Qy	515	LQ	516
Db	515	LO	516

## RESULT 10

095262	PRELIMINARY;	PRT;	518 AA.
ID	Q95262		
AC	Q95262;		
DT	01-FEB-1997 (fREMBLrel. 02, Created)		
DT	01-FEB-1997 (fREMBLrel. 02, Last sequence update)		
DT	01-MAR-2003 (fREMBLrel. 23, Last annotation update)		
DE	CaM kinase II gamma B (Calcium/calmodulin-dependent protein kinase II isoform gamma-B)		
DE	Muscula putorius furo (Ferret), and		
OS	Sus scrofa (Pig).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;		
OC	Muscula.		
CC	NCBI_TaxID=9669, 9823;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	SPECIES=M. putorius furo;		
RC	Gangopadhyay S.S., Morgan K.G.;		
RA	"CaM Kinase II Gamma Isoforms of Ferret."		
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.		
RL	[2]		
RP	SEQUENCE FROM N.A.		
RC	SPECIES=frog; TISSUE=Aortic smooth muscle;		
RC	MEDLINE=97238879; PubMed=9083077;		
RA	Singer H.A., Benschoter H.A., Schworer C.M.;		
RT	"Novel Ca2+/calmodulin-dependent protein kinase II gamma-subunit variants expressed in vascular smooth muscle, brain, and cardiomyocytes."		
RT	J. Biol. Chem. 272:9393-9400(1997).		
CC	!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.		
CC	EMBL; AF464184; AAL69955.1; -		
DR	EMBL; U72970; AAC48711.1; -		
DR	HSSP; Q63450; 1A06.		
DR	InterPro; IPR000719; Prot_kinase.		
DR	InterPro; IPR002290; Ser_thr_kinase.		
DR	Pfam; PF00069; pkinase; 1.		
DR	ProDom; PD000001; Prot_kinase; 1.		
DR	SMART; SM00220; S_TKc; 1.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.		
DR	PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.		
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.		
KW	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.		
SC	SEQUENCE 518 AA; 58365 MW; 127250AF541196BF CRC64;		
Query Match	82.1%; Score 2230; DB 6; Length 518;		
Best Local Similarity	79.2%; Pred. No. 9.5e-170;		
Matches 430; Conservative 25; Mismatches 36; Indels 52; Gaps 4			
QY	1 MATVTCRFTDVLVDYEDIGKGFVSVRCVKLCPTGHEYAAKLTNKKLSARDHOKLER 60		
DB	1 MATATCTRFTDDIQLEELGKGFVSVRCVKKSTQEYAAKLTNKKLSARDHOKLER 60		
QY	61 EARICRLKHSNIVRLHSDISEGPHYLVFDLTGGELFDIVAREYSEADASHCIQI 120		
DB	61 EARICRLKHSNIVRLHSDISEGPHYLVFDLTGGELFDIVAREYSEADASHCIHQI 120		
QY	121 LEAVLHCHQMGVHRODKPENLLASKCKGAAYKLADFGIALEIVQGDQAWGEGAGTPGY 240		
DB	121 LGSVNIHQHDIHVRDOKPENLLASKCKGAAYKLADFGIALEIVQGDQAWGEGAGTPGY 240		
QY	181 LSPVLRLKAYGKPDVIWACGVILYLLVGYPPFDWEDQHLKIQIKAGAYDFSPSPWDT 240		
DB	181 LSPVLRLKDPYKPKVDIWACGVILYLLVGYPPFDWEDQHLKIQIKAGAYDFSPSPWDT 240		
QY	241 VTPKLNINOMLTINPAKRIITAEALKHEWVCQQRSTVASMHHROETVECLKKFNRRKL 300		

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Db 241 VTPEAKNLINQMLTINPAKRITADQALKHPWQORSTVSMHMRQETVECLRKFNARRKL 300
QY 301 KGAILTMTLATRNFSVGRQTTAPATMTAAAGTMTGLVBOAKSLNKKAD-GVKPQNST 359
Db 301 KGAILTMTLATRNFSVGRQTTAPATMTAAAGTMTGLVBOAKSLNKKAD-GVKPQNST 359
Db 301 KGAILTMTLATRNFSVGRQTTAPATMTAAAGTMTGLVBOAKSLNKKAD-GVKPQNST 359
QY 360 KNSAAATSPKGLTPPAALPQPTVTHNPFVGIKESDSANTTTEDEDAKAKQELIKTTE 419
Db 336 KNSLVSPAQAPLQATAMEPQTIVVHNATDGIKGSNTTTEDEDLKVRKQELIKTE 395
QY 420 QLIEAVNNGDFEAYA-----FYFNLLAKNSKSIPIHTTIL 453
Db 396 QLIEALNNGDFEAYATKIDPGLTSPPEALGNLVGMDHKFYFNLLAKNSKSIPIHTTIL 455
QY 454 NPHVHVIGEDACIATIRLTQIDQGRPTSQSETRVWHRDQKQWNVHFGSGAPVA 513
Db 456 NPHVHVIGEDACIATIRLTQIDQGRPTSQSETRVWHRDQKQWNVHFGSGAPAA 515
QY 514 PLQ 516
Db 516 PLQ 518

RESULT 11
Q9DFZ8
ID Q9DFZ8 PRELIMINARY; PRT; 643 AA.
AC Q9DFZ8;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase II gamma M subunit.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP TISSUE=Ovary;
RC "Differential expression of new calcium/calmodulin-dependent protein
RT kinase II isoforms during Xenopus laevis oocyte maturation.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -/- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=99070057; PubMed=9852955;
RA Takeuchi M., Fujisawa H.;
RT "New alternatively spliced variants of calmodulin-dependent protein
RT kinase II from rabbit liver.";
RL Gene 221:107-115(1998).
CC -/- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; D14905; BAA28869.1; -
DR HSP; O63450; 1A06.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 643 AA; 71486 MW; FEA517FD0D0037C6E CRC64;

Query Match 82.0%; Score 2225.5; DB 13; Length 643;
Best Local Similarity 68.5%; Pred. No. 3e-159;
Matches 445; Conservative 28; Mismatches 36; Indels 141; Gaps 8;

QY 1 MATTVTCTRTFDEYQYIEDIGKGFVSVVRCVKLTGHEYAAKIINTKLSARDHOKLER 60
Db 1 MATTVTCTRTFDEYQYIEDIGKGFVSVVRCVKLTGHEYAAKIINTKLSARDHOKLER 60
QY 61 EARIICLLKNSVIRLHDSISEGPHYLVDLYVTGGELFEDIYAREYISEADASHCTQOI 120
Db 61 EARIICLLKNSVIRLHDSISEGPHYLVDLYVTGGELFEDIYAREYISEADASHCTQOI 120
QY 121 LEAVLHCHQMGVVRHRLKFNLLAKSKCKGAANKVADFGLAIEVQDQQAQWFGAGTGGY 180
Db 121 LEAVLHCHQMGVVRHRLKFNLLAKSKCKGAANKVADFGLAIEVQDQQAQWFGAGTGGY 180

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QY 181 LSPFVLKEAYGKPVDIWACGVYLLVGYPPFNDQHKLYQOIKAGAYDPPSPENDT 240
Db 181 LSPFVLKEAYGKPVDIWACGVYLLVGYPPFNDQHKLYQOIKAGAYDPPSPENDT 240
QY 241 VTPEAKNLINQMLTINPAKRITAEALKHPWQORSTVSMHMRQETVECLRKFNARRKL 300
Db 241 VTPEAKNLINQMLTINPAKRITAEALKHPWQORSTVSMHMRQETVECLRKFNARRKL 300
QY 301 KGAILTMTLATRNFS-----VGRQTAPATMTAAAGTMT 335
Db 301 KGAILTMTLATRNFSVGRQTTAPATMTAAAGTMTITGVGRQTSAPVVAATSA 356
QY 336 GLVBO-AKSLNKKADGVKQPTNSTKNSAATSPKCTLPP--AALEPQTTVHNPFVDGK 392
Db 337 NLVBOAKSLNKKADGVKQPTNN-KNS--IISPAKENPPLQASMEPQTTVVHNATDGK 413
QY 393 ESSDSANTTTEDEDAK-----FYFNLLAKNSKSIPIHTTILNPHVHVIGEDAAC 409
Db 414 GSTESCNITTDEDEDLKANVCPGDPGLLQGWQSESKIQTESLQSQIGLWGSSTAQSC 473
QY 410 -----RKQELIKTTEDEDAKAKQELIKTTEDEDAK 432
Db 474 KTLANDSPGQTLLEPAQSEPMPLTPVVPFSLNSLLRKQELIKTTEDEDAK 533
QY 433 YA-----FYFNLLAKNSKSIPIHTTILNPHVHVIGEDAAC 466
Db 534 YTKIDPGLTSPPEALGNLVGMDHKFYFNLLAKNSKSIPIHTTILNPHVHVIGEDAAC 593
QY 467 IAYIRLQYIDQGRPTSQSETRVWHRDQKQWNVHFGSGAPVAPLQ 516
Db 594 IAYIRLQYIDQGRPTSQSETRVWHRDQKQWNVHFGSGAPVAPLQ 643

RESULT 12
O77707
ID O77707 PRELIMINARY; PRT; 518 AA.
AC O77707;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Calmodulin-dependent protein kinase II-gamma dash2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=99070057; PubMed=9852955;
RA Takeuchi M., Fujisawa H.;
RT "New alternatively spliced variants of calmodulin-dependent protein
RT kinase II from rabbit liver.";
RL Gene 221:107-115(1998).
CC -/- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; D14905; BAA28869.1; -
DR HSP; O63450; 1A06.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 518 AA; 59348 MW; 66614030ACE34BD CRC64;

Query Match 81.9%; Score 2223; DB 6; Length 518;
Best Local Similarity 78.9%; Pred. No. 3.5e-169;
Matches 430; Conservative 23; Mismatches 36; Indels 56; Gaps 5;

QY 1 MATTVTCTRTFDEYQYIEDIGKGFVSVVRCVKLTGHEYAAKIINTKLSARDHOKLER 60

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Db 1 MATATCTRTDDYQLFEEELGKGF SVVRCVKKSTQEIYAAKIINTKKLSARDHOKLER 60
QY 61 EARICRLKHSNIVRLHDSISEEGFHYLVFDLVTGGELFEDIVAREYYSADASHCICQI 120
Db 61 EARICRLKHPNIVRLHDSISEEGFHYLVFDLVTGGELFEDIVAREYYSADASHCICQI 120
QY 121 LEAVLCHOMGVVHRDLKPENLLASCKGAAVKLADFGLAIEVQGGQAAWFGAGTGGY 180
Db 121 LESVNHQHDIVHRDLKPENLLASCKGAAVKLADFGLAIEVQGGQAAWFGAGTGGY 180
QY 181 LSPVLKRAYGKPYDINACGVILY ILLVGYPPFWDEQHKLYQQIKAGAYDPPSPEDWT 240
Db 181 LSPVLKRAYGKPYDINACGVILY ILLVGYPPFWDEQHKLYQQIKAGAYDPPSPEDWT 240
QY 241 VTPKAKLINQMLTINPAKRITAEALKHPWCORSTVASMMHROETVECLKFNARRKL 300
Db 241 VTPKAKLINQMLTINPAKRITADQALKHPWCORATVASMMHROETVECLKFNARRKL 300
QY 301 KGALLTMTLATRNFSVGRTQATPATMTSTAASGTTMGLVEQAKSLNKKAD-GYKPTNST 359
Db 301 KGALLTMTLVSRNFS-----AKSLNKKSDGGYKPSN-- 334
QY 360 KNSAAPSFGTLPP--AALPQTQTVIHNVDGIKESSDSANTTIEDAKAKQBIKT 417
Db 335 -NKISLVSPAQEPAPLQAMEPQTQTVVHNATDGIKSTESCTTTEDDLKVRKQBIKI 393
QY 418 TEQLIEAVNNGDEAVA-----FVENLAKNSKPIHTT 451
Db 394 TEQLIEAVNNGDEAVA-----FVENLAKNSKPIHTT 453
QY 452 ILNPHVHVIGEDAACIAYIRLTQYIDGGQRPRTSQSEETRVWHRRDQKWNVHFCGAP 511
Db 454 ILNPHVHVIGEDAACIAYIRLTQYIDGGQRPRTSQSEETRVWHRRDQKWNVHFCGAP 513
QY 512 VAPLQ 516
Db 514 AAPLQ 518

RESULT 13
Q9DG01 PRELIMINARY; PRT; 541 AA.
ID Q9DG01 AC Q9DG01; ID Q9DG01 PRELIMINARY; PRT; 541 AA.
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase II gamma J subunit.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Stevens I., Rondelez E., Merlevede W., Goris J.;
RT "Differential expression of new calcium/calmodulin-dependent protein
kinase II isoforms during Xenopus laevis oocyte maturation.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF233630; AAG17555.1; -.
DR HSP; Q63450; 1A06
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 541 AA; 60586 MW; 7B071C5DA7001B59 CRC64;

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Query Match 81.6%; Score 2214.5; DB 13; Length 541;
Best Local Similarity 75.7%; Pred. No. 1.8e-168;
Matches 431; Conservative 25; Mismatches 32; Indels 81; Gaps 5;

QY 1 MATVTCTRTDEYQVLEEDIGKGF SVVRCVKKSTQEIYAAKIINTKKLSARDHOKLER 60
Db 1 MATPTCTRTDEYQVLEEDIGKGF SVVRCVKKSTQEIYAAKIINTKKLSARDHOKLER 60
QY 61 EARICRLKHSNIVRLHDSISEEGFHYLVFDLVTGGELFEDIVAREYYSADASHCICQI 120
Db 61 EARICRLKHPNIVRLHDSISEEGFHYLVFDLVTGGELFEDIVAREYYSADASHCICQI 120
QY 121 LEAVLCHOMGVVHRDLKPENLLASCKGAAVKLADFGLAIEVQGGQAAWFGAGTGGY 180
Db 121 LESVNHQHDIVHRDLKPENLLASCKGAAVKLADFGLAIEVQGGQAAWFGAGTGGY 180
QY 181 LSPVLKRAYGKPYDINACGVILY ILLVGYPPFWDEQHKLYQQIKAGAYDPPSPEDWT 240
Db 181 LSPVLKRAYGKPYDINACGVILY ILLVGYPPFWDEQHKLYQQIKAGAYDPPSPEDWT 240
QY 241 VTPKAKLINQMLTINPAKRITAEALKHPWCORSTVASMMHROETVECLKFNARRKL 300
Db 241 VTPKAKLINQMLTINPAKRITADQALKHPWCORSTVASMMHROETVECLKFNARRKL 300
QY 301 KGALLTMTLATRNFSVGRTQATPATMTSTAASGTTMGLVEQAKSLNKKAD-GYKPTNST 334
Db 301 KGALLTMTLVSRNFSGTAFCRKAASVTCTSTGDTTITGVGRTQSA PVVAATSA-- 357
QY 335 MGLVQD-AKSLNKKADGVQPTNSTKNSAATSPKTLPPAALPQTQTVIHNVDGIKE 393
Db 358 -NLVEQAQAKSLNKKTDGVK-----EPQTTVHNATDGIK 392
QY 394 SDSANTTIEDAKAKQBIKTTEQLIEAVNNGDEAVA----- 434
Db 393 STESNTTIEDDLKVRKQBIKIITEQLIEAVNNGDEAVA----- 452
QY 435 -----FVENLAKNSKPIHTTILNPHVHVIGEDAACIAYIRLTQYIDGGQRPRTSQS 487
Db 453 EGMDFEKFYFDNLLSKTKPIHTTILNPHVHVIGEDAACIAYIRLTQYIDGGQRPRTSQS 512
QY 488 EETRVWHRRDQKWNVHFCGAPVAPLQ 516
Db 513 EETRVWHRRDQKWNVHFCGAPVAPLQ 541

RESULT 14
Q8CAC5 PRELIMINARY; PRT; 512 AA.
ID Q8CAC5 AC Q8CAC5; ID Q8CAC5 PRELIMINARY; PRT; 512 AA.
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase II.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK039076; BAC30232.1; -.
SQ SEQUENCE 512 AA; 57777 MW; E5E51B5F820D63B0 CRC64;

Query Match 81.2%; Score 2204; DB 11; Length 512;
Best Local Similarity 78.6%; Pred. No. 1.1e-167;
Matches 425; Conservative 29; Mismatches 31; Indels 56; Gaps 6;

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QY 1 MATVTCTRTFTDQYEDIGKGFVVRRCVKLTGHEVYAAKIINTKKLSARDHOKLER 60  
 Db 1 MASTTTCRTFTDQYEDIGKGFVVRRCVKLTGHEVYAAKIINTKKLSARDHOKLER 60  
 QY 61 EARIICRLKHSNIVRLHDSISEGPHYLVDLVGTGGELEFEDIVAREYIYSEADASHCQIQI 120  
 Db 61 EARIICRLKHSNIVRLHDSISEGPHYLVDLVGTGGELEFEDIVAREYIYSEADASHCQIQI 120  
 QY 121 LEAVLHCHQMGVVRHDLKPNENLLASKCKGAAYKVLADFGLAIEVQDQQAQWFGAGTPGY 180  
 Db 121 LEAVLHCHQMGVVRHDLKPNENLLASKCKGAAYKVLADFGLAIEVQDQQAQWFGAGTPGY 180  
 QY 181 LSPVLRKEAYGKPVDIWAGVILYLLVGPFPWEDDQHKLYQOIKAGAYDFSPSWDT 240  
 Db 181 LSPVLRKEAYGKPVDIWAGVILYLLVGPFPWEDDQHKLYQOIKAGAYDFSPSWDT 240  
 QY 241 VTPKAKNLINOMLTINPAKRITAEALKHPWVQCORSTVASMHRQETVECLKKNARRKL 300  
 Db 241 VTPKAKNLINOMLTINPAKRITAEALKHPWVQCORSTVASMHRQETVECLKKNARRKL 300  
 QY 301 KGAILTTMLATRNFSVGRQTTPATMSTAASGTMGLVEQAKSLNKKKADGVKQPTNSTK 360  
 Db 301 KGAILTTMLATRNFSVGRQTTPATMSTAASGTMGLVEQAKSLNKKKADGVKQPTNSTK 360  
 QY 361 NSAAATSPKGLTPPAALEPQTTVIHNPVDGKIKSSDSANTTIEDAKARQEIITKTEQ 420  
 Db 361 NSAAATSPKGLTPPAALEPQTTVIHNPVDGKIKSSDSANTTIEDAKARQEIITKTEQ 420  
 QY 455 PHVHVIGEDAACIAYIRLQYIDGGRPRTSQSETRVWHRDQKQWNVHFCSGAPVAP 514  
 Db 455 PHVHVIGEDAACIAYIRLQYIDGGRPRTSQSETRVWHRDQKQWNVHFCSGAPVAP 514  
 QY 515 L 515  
 Db 511 I 511

RESULT 15

Q95263 PRELIMINARY; PRT; 495 AA.  
 AC Q95263;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE CaM kinase II gamma C-1 (Calcium/calmodulin-dependent protein kinase  
 II isoform gamma-C protein kinase II).  
 OS Mustela putorius furo (Ferret), and  
 Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;  
 OC Mustela.  
 OX NCBI\_TaxID=9669, 9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=M. putorius furo;  
 RA Gangopadhyay S. S., Morgan K. G.;  
 FT "CaM Kinase II Gamma isoforms of Ferret."  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Pig; TISSUE=Aortic smooth muscle;  
 RX MEDLINE=97238879; PubMed=9083077;  
 RA Singer H.A., Benschoter H.A., Schworer C.M.;  
 RT "Novel Ca2+/calmodulin-dependent protein kinase II gamma-subunit  
 variants expressed in vascular smooth muscle, brain, and  
 cardiomyocytes."  
 RT J. Biol. Chem. 272:9393-9400(1997).  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DB EMBL; AF464182; AAL69933.1; -.

DR EMBL; U72971; AAC48712.1; -.  
 DR HSP; Q63450; IAO6.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00101; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 495 AA; 55960 MW; 168EA409723DF4C4 CRC64;  
 Query Match 80.5%; Score 2186.5; DB 6; Length 495;  
 Best Local Similarity 77.7%; Pred. No. 2.7e-166;  
 Matches 421; Conservative 19; Mismatches 29; Indels 73; Gaps 3;  
 QY 1 MATVTCTRTFTDQYEDIGKGFVVRRCVKLTGHEVYAAKIINTKKLSARDHOKLER 60  
 Db 1 MASTTTCRTFTDQYEDIGKGFVVRRCVKLTGHEVYAAKIINTKKLSARDHOKLER 60  
 QY 61 EARIICRLKHSNIVRLHDSISEGPHYLVDLVGTGGELEFEDIVAREYIYSEADASHCQIQI 120  
 Db 61 EARIICRLKHSNIVRLHDSISEGPHYLVDLVGTGGELEFEDIVAREYIYSEADASHCQIQI 120  
 QY 121 LEAVLHCHQMGVVRHDLKPNENLLASKCKGAAYKVLADFGLAIEVQDQQAQWFGAGTPGY 180  
 Db 121 LEAVLHCHQMGVVRHDLKPNENLLASKCKGAAYKVLADFGLAIEVQDQQAQWFGAGTPGY 180  
 QY 181 LSPVLRKEAYGKPVDIWAGVILYLLVGPFPWEDDQHKLYQOIKAGAYDFSPSWDT 240  
 Db 181 LSPVLRKEAYGKPVDIWAGVILYLLVGPFPWEDDQHKLYQOIKAGAYDFSPSWDT 240  
 QY 241 VTPKAKNLINOMLTINPAKRITAEALKHPWVQCORSTVASMHRQETVECLKKNARRKL 300  
 Db 241 VTPKAKNLINOMLTINPAKRITAEALKHPWVQCORSTVASMHRQETVECLKKNARRKL 300  
 QY 301 KGAILTTMLATRNFSVGRQTTPATMSTAASGTMGLVEQAKSLNKKKADGVKQPTNSTK 360  
 Db 301 KGAILTTMLATRNFSVGRQTTPATMSTAASGTMGLVEQAKSLNKKKADGVKQPTNSTK 360  
 QY 361 NSAAATSPKGLTPPAALEPQTTVIHNPVDGKIKSSDSANTTIEDAKARQEIITKTEQ 420  
 Db 361 NSAAATSPKGLTPPAALEPQTTVIHNPVDGKIKSSDSANTTIEDAKARQEIITKTEQ 420  
 QY 421 LIEAVNNGDFEAYA-----FYFENLLAKNSKPIHTTILN 454  
 Db 421 LIEAVNNGDFEAYA-----FYFENLLAKNSKPIHTTILN 454  
 QY 455 PHVHVIGEDAACIAYIRLQYIDGGRPRTSQSETRVWHRDQKQWNVHFCSGAPVAP 514  
 Db 455 PHVHVIGEDAACIAYIRLQYIDGGRPRTSQSETRVWHRDQKQWNVHFCSGAPVAP 514  
 QY 515 LQ 516  
 Db 494 LQ 495

Search completed: October 10, 2003, 08:10:36

Job time : 116 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 10, 2003, 08:06:36 ; Search time 26 Seconds  
(without alignments)  
839.708 Million cell updates/sec

Title: US-09-820-790B-2  
Perfect score: 2715  
Sequence: 1 MATTVTCTRTDEYQLYEDI.....DGKQNVHFCGAPVAPLQ 516

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2.6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2.6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2.6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2.6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2.6/ptodata/1/iaa/PTCUS\_COMB.pep.\*  
6: /cgn2.6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2225.5	82.0	565	4	US-09-800-960-2
2	2205	81.2	556	4	US-09-800-960-4
3	1450	53.4	295	1	US-07-951-715A-23
4	1450	53.4	295	2	US-08-459-448A-23
5	1450	53.4	295	3	US-08-459-595A-23
6	1450	53.4	295	3	US-08-459-504B-23
7	1450	53.4	295	3	US-08-459-444-23
8	1450	53.4	295	4	US-09-547-422-23
9	1405	51.7	264	2	US-07-857-224B-19
10	1294	47.7	264	2	US-07-857-224B-18
11	619.5	22.8	355	4	US-09-579-664B-10
12	583	21.5	370	2	US-08-878-989-19
13	583	21.5	370	3	US-09-272-796-19
14	583	21.5	370	4	US-09-457-040B-31
15	582	21.4	765	4	US-09-975-326-4
16	582	21.4	766	4	US-09-975-326-2
17	558	20.6	463	1	US-07-951-715A-25
18	558	20.6	463	3	US-08-459-448A-25
19	558	20.6	463	3	US-08-459-595A-25
20	558	20.6	463	3	US-08-459-504B-25
21	558	20.6	463	3	US-08-459-444-25
22	558	20.6	463	4	US-09-547-422-25
23	556.5	20.5	424	2	US-08-715-568A-1
24	549	20.2	639	3	US-09-347-801-17
25	546	20.1	501	4	US-09-734-030-2
26	542.5	20.0	343	2	US-08-878-989-5
27	542.5	20.0	343	3	US-09-272-796-5

28	540.5	19.9	464	1	US-07-951-715A-22	Sequence 22, Appl
29	540.5	19.9	464	2	US-08-459-448A-22	Sequence 22, Appl
30	540.5	19.9	464	3	US-08-459-595A-22	Sequence 22, Appl
31	540.5	19.9	464	3	US-08-459-504B-22	Sequence 22, Appl
32	540.5	19.9	464	3	US-08-459-444-22	Sequence 0, Appl
33	540.5	19.9	464	4	US-09-547-422-22	Sequence 0, Appl
34	529	19.5	456	1	US-08-464-164-2	Sequence 2, Appl
35	529	19.5	456	1	US-08-338-057-2	Sequence 2, Appl
36	529	19.5	456	2	US-08-668-416-2	Sequence 2, Appl
37	524	19.3	520	4	US-09-257-825B-20	Sequence 20, Appl
38	521.5	19.2	387	1	US-08-713-828-3	Sequence 3, Appl
39	521.5	19.2	387	2	US-08-919-627-3	Sequence 3, Appl
40	521.5	19.2	387	2	US-09-096-245-3	Sequence 3, Appl
41	521.5	19.2	387	4	US-09-457-040B-30	Sequence 30, Appl
42	515.5	19.0	388	1	US-08-713-828-5	Sequence 5, Appl
43	515.5	19.0	388	2	US-08-919-627-5	Sequence 5, Appl
44	515.5	19.0	388	2	US-09-096-245-5	Sequence 5, Appl
45	512	18.9	264	2	US-07-857-224B-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1  
US-09-800-960-2  
; Sequence 2, Application US/09800960  
; Patent No. 6387677  
; GENERAL INFORMATION:  
; APPLICANT: YE, Jane et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001158  
; CURRENT APPLICATION NUMBER: US/09/800,960  
; CURRENT FILING DATE: 2001-03-08  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 565  
; TYPE: PRT  
; ORGANISM: Human  
US-09-800-960-2

Query Match	82.0%;	Score	2225.5;	DB 4;	Length	565;			
Best Local Similarity	74.7%;	Pred. No.	1.1e-204;						
Matches	434;	Conservative	30;	Mismatches	36;	Indels	81;	Gaps	5;
QY	1	MATVTCTRTDEYQLYEDI	IGKAFSVVRCVKLTG	HEYAAKII	NTKLSARDHQKLER	60			
DB	1	MATTATCTRTDDYQLFEELGKAFSVVRCVKLTG	HEYAAKII	NTKLSARDHQKLER	60				
QY	61	EARICRLKHSNIVRLHDSISEGPHYLVFDLVTGGELFEDIVAREY	YSEADASHCICQI	120					
DB	61	EARICRLKHPNIVRLHDSISEGPHYLVFDLVTGGELFEDIVAREY	YSEADASHCICQI	120					
QY	121	LEAVLEHCHQMGVVHRDLKPNLLASKCKGA	AVKADFGLAIEVQDQQA	NFAGTPTGY	180				
DB	121	LESVNHIIHQHDI	VHRDLKPNLLASKCKGA	AVKADFGLAIEVQDQQA	NFAGTPTGY	180			
QY	181	LSPEVLRKEATGKPYDI	WACGVYILLYGYP	PPWDEQHKLYQOI	KAGAYDFP	240			
DB	181	LSPEVLRKDPYKPYDI	WACGVYILLYGYP	PPWDEQHKLYQOI	KAGAYDFP	240			
QY	241	VTPKAKNLINOMLTINPAKRITAEAL	KHPWVCORSTVASMHRQETV	CLKFNARKL	300				
DB	241	VTPKAKNLINOMLTINPAKRITADQAL	KHPWVCORSTVASMHRQETV	CLKFNARKL	300				
QY	301	KGAITTMATRNFSVGRQTPATMSTA	ASGTTMGLVEQAKSLNKKAD	-GVKPTQNST	359				
DB	301	KGAITTMATRNFSVGRQTPATMSTA	ASGTTMGLVEQAKSLNKKAD	-GVKPTQNST	359				
QY	360	KNSAATSPKGLTPPAALPEQTVIHN	PDGIKSSDSANTTIEDAKA	-----	409				
DB	360	KNSAATSPKGLTPPAALPEQTVIHN	PDGIKSSDSANTTIEDAKA	-----	409				

Db 358 S-----VHMEPQTYYVHNATDGIKGTSTESCTNTTDEDKKAAPLRTGNGSS 404

QY 410 -----RKOEIKTKTEOLIEAVNNGDFEAYA----- 434

Db 405 VPEGSSDRTPASAGMQPQPSLCSSAMRKQEIITKITEOLIEAINNGDFEAYIKICDPGL 464

QY 435 -----FYFENLLAKNSKPIHTTILNPHVHVHIGEDACIAYIRLTOY 475

Db 465 TSFEPEALNLEVGMDHFHYFENLLSKNSKPIHTTILNPHVHVHIGEDACIAYIRLTOY 524

QY 476 IDGGRPTSSQSEETRWHRDQKQWNVHFCGAPVAPLQ 516

Db 525 IDGGRPTSSQSEETRWHRDQKQWNVHFCGAPVAPLQ 565

RESULT 2

US-09-800-960-4

; Sequence 4, Application US/09800960

; Patent No. 6387677

; GENERAL INFORMATION:

; APPLICANT: YE, Jane et al.

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; FILE REFERENCE: C1001158

; CURRENT APPLICATION NUMBER: US/09/800,960

; CURRENT FILING DATE: 2001-03-08

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 556

; TYPE: PRT

; ORGANISM: Human

US-09-800-960-4

Query Match 81.2%; Score 2205; DB 4; Length 556;

Best Local Similarity 74.2%; Pred. No. 1e-202;

Matches 431; Conservative 25; Mismatches 35; Indels 90; Gaps 5;

QY 1 MATTTTCFRFFDEYQVLEIDGKGFAPSVVRCVKLCTGHEYAAKINTKLSARDHOKLER 60

Db 1 MATTTATCFRFFDDYQVLEELGKGFAPSVVRCVKLTQEFYAAKINTKLSARDHOKLER 60

QY 61 EARICRLKHSNIVRLHDSISEGPHYLVDLVTGSELFEDIVAREYTYSEADASHCITQI 120

Db 61 EARICRLKHSNIVRLHDSISEGPHYLVDLVTGSELFEDIVAREYTYSEADASHCITQI 120

QY 121 LEAVLHCHOMGVVHRDLKPNILLASKCKGAAGVADGLAEIVGQDOQAWFGAGTPGY 180

Db 121 LESVNHIEQHDIVHRDLKPNILLASKCKGAAGVADGLAEIVGQDOQAWFGAGTPGY 180

QY 181 LSPFVRKEAYGKPDVWAGGVILYLVGPPPWEDDQHKLYQKIKAGAYDFPSPWD 240

Db 181 LSPFVLRKDPYKPDVWAGGVILYLVGPPPWEDDQHKLYQKIKAGAYDFPSPWD 240

QY 241 VTPEAKNLINMLTINPAKRIAHALKHPWCORSTVASMMHQRQTEVCKLKNARRKL 300

Db 241 VTPEAKNLINMLTINPAKRIADQALHPWCORSTVASMMHQRQTEVCKLKNARRKL 300

QY 301 KGAILTMTATRNFSVGRQTTAPATMSTAASGTTMGLVQAKSLNKKAD-GVYPOPNST 359

Db 301 KGAILTMTATRNFSVGRQTTAPATMSTAASGTTMGLVQAKSLNKKAD-GVYPOPNST 359

QY 360 KNSAATSPKGTLPAPALEPQTVVHNPDGKIKSSDSANTTIEDAKA----- 409

Db 360 KNSLSPAQEPAPLQATMEPQTVVHNATDGIKGTSTESCTNTTDEDKKAAPLRTGNGSS 395

QY 410 -----RKOEIKTKTEOLIEAVNNGDFEAYA----- 434

Db 396 VPEGSSDRTPASAGMQPQPSLCSSAMRKQEIITKITEOLIEAINNGDFEAYIKICDPGL 455

QY 435 -----FYFENLLAKNSKPIHTTILNPHVHVHIGEDACIAYIRLTOY 475

Db 456 TSFEPEALNLEVGMDHFHYFENLLSKNSKPIHTTILNPHVHVHIGEDACIAYIRLTOY 515

QY 476 IDGGRPTSSQSEETRWHRDQKQWNVHFCGAPVAPLQ 516

Db 516 IDGGRPTSSQSEETRWHRDQKQWNVHFCGAPVAPLQ 556

RESULT 3

US-07-951-715A-23

; Sequence 23, Application US/07951715A

; Patent No. 5625136

; GENERAL INFORMATION:

; APPLICANT: Koziel, Michael G.

; APPLICANT: Desai, Malini M.

; APPLICANT: Lewis, Kelly S.

; APPLICANT: Kramer, Vance C.

; APPLICANT: Warren, Gregory W.

; APPLICANT: Evola, Stephen V.

; APPLICANT: Crossland, Lyle D.

; APPLICANT: Wright, Martha S.

; APPLICANT: Merlin, Ellis J.

; APPLICANT: Launis, Karen L.

; APPLICANT: Rothstein, Steven J.

; APPLICANT: Bowman, Cindy G.

; APPLICANT: Dawson, John L.

; APPLICANT: Dunder, Erik M.

; APPLICANT: Pace, Gary M.

; APPLICANT: Suttie, Janet L.

; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CIBA-GEIGY Corporation

; STREET: 7 Skyline Drive

; CITY: Hawthorne

; STATE: New York

; COUNTRY: USA

; ZIP: 10532

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30B

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/951,715A

; FILING DATE: 25-SEP-1992

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/772,027

; FILING DATE: 04-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Spruill, W. Murray

; REGISTRATION NUMBER: 32,943

; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (919)541-8615

; TELEFAX: (919)541-8689

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 295 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHEICAL: NO

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..295

; OTHER INFORMATION: /note= "rat protein kinase II

; OTHER INFORMATION: protein sequence as shown in Figure 32."

US-07-951-715A-23

Query Match 53.4%; Score 1450; DB 1; Length 295;

```

; Best Local Similarity 92.5%; Pred. No. 9.6e-131;
; Matches 273; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 14 YQYEDIGKGAFAVVRVCVKLTGHEHYAAKIINTKLSARDHQKLEREARICRLKHSNI 73
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 YQFEEELGKGAFAVVRVCVKLTGHEHYAAKIINTKLSARDHQKLEREARICRLKHPNI 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 74 VRLHDSISEGFGHYLVFDLVTGGELFEDIVAREYYSADASHCICQIILEAVLHCHQGVV 133
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 VRLHDSISEGFGHYLVFDLVTGGELFEDIVAREYYSADASHCICQIILEAVLHCHQDI 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 134 HRDLKPENLLASCKGAAGVADGLALEVQGGQAAFGFAGTGCYLSPEVLRKEAYGK 193
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 HRDLKPENLLASCKGAAGVADGLALEVQGGQAAFGFAGTGCYLSPEVLRKDPYGK 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 194 PVDIWACGVILYLLVGYPPFWDQHKLYQOIKAGAYDFPSPEDWTVTPEAKNLINQML 253
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 PVDIWACGVILYLLVGYPPFWDQHKLYQOIKAGAYDFPSPEDWTVTPEAKNLINQML 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 254 TINPAKRITAEALKHFWQVQCRSTVASMHRQETVECLKFNARRKLGAILTTM 308
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 TINPAKRITADQALKHFWQVQCRSTVASMHRQETVECLKFNARRKLGAILTTM 295
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
US-08-459-448A-23
; Sequence 23, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttle, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5859336artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd., POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,448A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.

```

```

; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 295 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; NAME/KEY: Protein
; LOCATION: 1..295
; OTHER INFORMATION: /note= "rat protein kinase II
; OTHER INFORMATION: protein sequence as shown in Figure 32."
US-08-459-448A-23

Query Match 53.4%; Score 1450; DB 2; Length 295;
Best Local Similarity 92.5%; Pred. No. 9.6e-131;
Matches 273; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 14 YQYEDIGKGAFAVVRVCVKLTGHEHYAAKIINTKLSARDHQKLEREARICRLKHSNI 73
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 YQFEEELGKGAFAVVRVCVKLTGHEHYAAKIINTKLSARDHQKLEREARICRLKHPNI 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 74 VRLHDSISEGFGHYLVFDLVTGGELFEDIVAREYYSADASHCICQIILEAVLHCHQGVV 133
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 VRLHDSISEGFGHYLVFDLVTGGELFEDIVAREYYSADASHCICQIILEAVLHCHQDI 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 134 HRDLKPENLLASCKGAAGVADGLALEVQGGQAAFGFAGTGCYLSPEVLRKEAYGK 193
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 HRDLKPENLLASCKGAAGVADGLALEVQGGQAAFGFAGTGCYLSPEVLRKDPYGK 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 194 PVDIWACGVILYLLVGYPPFWDQHKLYQOIKAGAYDFPSPEDWTVTPEAKNLINQML 253
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 PVDIWACGVILYLLVGYPPFWDQHKLYQOIKAGAYDFPSPEDWTVTPEAKNLINQML 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 254 TINPAKRITAEALKHFWQVQCRSTVASMHRQETVECLKFNARRKLGAILTTM 308
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 TINPAKRITADQALKHFWQVQCRSTVASMHRQETVECLKFNARRKLGAILTTM 295
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
US-08-459-595A-23
; Sequence 23, Application US/08459595A
; Patent No. 6018104
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttle, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6018104artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd., POB 2005

```

CITY: Tarrytown  
STATE: New York  
COUNTRY: USA  
ZIP: 10591-9005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,595A  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Pace, Gary M.  
REGISTRATION NUMBER: 40403  
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8582  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 295 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
NAME/KEY: Protein  
LOCATION: 1..295  
OTHER INFORMATION: /note= "rat protein kinase II  
OTHER INFORMATION: protein sequence as shown in Figure 32."  
US-08-459-595A-23

Query Match 53.4%; Score 1450; DB 3; Length 295;  
Best Local Similarity 92.5%; Pred. No. 9.6e-131;  
Matches 273; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 14 YQYEDIGKGFVVRVCVKLTCTGHEVYAAKIINTKLSARDHQKLEAREICRLKHSNI 73  
Db 1 YQFEELGKGFVVRVCVKLTCTGHEVYAAKIINTKLSARDHQKLEAREICRLKHPNI 60  
QY 74 VRLHDSISEEGFHYLFDLVTGGELFEDIVAREYISDASHCIQOILEAVLHCHQGVV 133  
Db 61 VRLHDSISEEGFHYLFDLVTGGELFEDIVAREYISDASHCIHQILESYNHINQHDIV 120  
QY 134 HRDLKPNLLASCKGAAYKADFGLEIVQGDQAWFGAGTGPYLSPEVLKRAYGK 193  
Db 121 HRDLKPNLLASCKGAAYKADFGLEIVQGDQAWFGAGTGPYLSPEVLKRDYK 180  
QY 194 PVDIWACGVILYLLVGYPPFDEQHKLYQOIKAGAYDPPSPEDVTPPAKNLNQML 253  
Db 181 PVDIWACGVILYLLVGYPPFDEQHKLYQOIKAGAYDPPSPEDVTPPAKNLNQML 240  
QY 254 TINPAKRITAEALKHPWCORSTVASMHRQETVECLKFNARRKLGAILTMM 308  
Db 241 TINPAKRITADQALKHPWCORSTVASMHRQETVECLKFNARRKLGAILTMM 295

## RESULT 6

US-08-459-504B-23  
; Sequence 23, Application US/08459504B  
; Patent No. 6075185  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.

APPLICANT: Lewis, Kelly S.  
APPLICANT: Kramer, Vance C.  
APPLICANT: Warren, Gregory W.  
APPLICANT: Evola, Stephen V.  
APPLICANT: Crossland, Lyle D.  
APPLICANT: Wright, Martha S.  
APPLICANT: Merlin, Ellis J.  
APPLICANT: Launis, Karen L.  
APPLICANT: Rothstein, Steven J.  
APPLICANT: Bowman, John L.  
APPLICANT: Dunder, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Suttie, Janet L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
FILING DATE: 25-SEP-1992  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6075185artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,504B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/459,595  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8587  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 295 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..295  
OTHER INFORMATION: /note= "rat protein kinase II  
OTHER INFORMATION: protein sequence as shown in Figure 32."  
US-08-459-504B-23  
Query Match 53.4%; Score 1450; DB 3; Length 295;  
Best Local Similarity 92.5%; Pred. No. 9.6e-131;  
Matches 273; Conservative 10; Mismatches 12; Indels 0; Gaps 0;  
QY 14 YQYEDIGKGFVVRVCVKLTCTGHEVYAAKIINTKLSARDHQKLEAREICRLKHSNI 73  
Db 1 YQFEELGKGFVVRVCVKLTCTGHEVYAAKIINTKLSARDHQKLEAREICRLKHPNI 60  
QY 74 VRLHDSISEEGFHYLFDLVTGGELFEDIVAREYISDASHCIQOILEAVLHCHQGVV 133

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Db      61 VRLHDSISEEGHYLVLDVTGGELFEDIVAREYVSEADASHCIHQILLESYNH1HQHDIV 120
QY      134 HRDLKPENLLASKCKGAAGVADGLAIEVQSGDQQAQWFGAGTGGYLSPEVLRKEAYGK 193
Db      121 HRDLKPENLLASKCKGAAGVADGLAIEVQSGDQQAQWFGAGTGGYLSPEVLRKDPYK 180
QY      194 PYDIWACGVILYLLVGYPPFWDQKHLYQOIKAGAYDPPSPWDVTPPAKLNINQML 253
Db      181 PYDIWACGVILYLLVGYPPFWDQKHLYQOIKAGAYDPPSPWDVTPPAKLNINQML 240
QY      254 TINPAKRITAEALKHPWQCORSTVASMHRQETVECLKFNARKLKGA1ITM 308
Db      241 TINPAKRITADQALKHPWQCORSTVASMHRQETVECLKFNARKLKGA1ITM 295

RESULT 7
US-08-459-444-23
; Sequence 23, Application US/08459444A
; Patent No. 6121014
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
;           Desai, Nalini M.
;           Lewis, Kelly S.
;           Kramer, Vance C.
;           Warren, Gregory W.
;           Evola, Stephen V.
;           Crossland, Lyle D.
;           Wright, Martha S.
;           Merlin, Ellis J.
;           Launis, Karen L.
; TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
;                   NUCLEIC ACID CODING SEQUENCE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESSES:
; ADDRESSSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,444A
; FILING DATE: 02-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 295 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..295
; OTHER INFORMATION: /note= "rat protein kinase II

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; protein sequence as shown in Figure 32."
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-08-459-444-23
Query Match      53.4%; Score 1450; DB 3; Length 295;
Best Local Similarity 92.5%; Pred. No. 9.6e-131;
Matches 273; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
QY      14 YOLYEDIGKAGSVRRVCVKLTGHEHYAAKIINTKKLSARHOKLEREARICILLKHSNI 73
Db      1 YOLFEELGKAGSVRRVCVKLTGHEHYAAKIINTKKLSARHOKLEREARICILLKHPNI 60
QY      74 VRLHDSISEEGHYLVLDVTGGELFEDIVAREYVSEADASHCIHQILLESYNH1HQHDIV 133
Db      61 VRLHDSISEEGHYLVLDVTGGELFEDIVAREYVSEADASHCIHQILLESYNH1HQHDIV 120
QY      134 HRDLKPENLLASKCKGAAGVADGLAIEVQSGDQQAQWFGAGTGGYLSPEVLRKEAYGK 193
Db      121 HRDLKPENLLASKCKGAAGVADGLAIEVQSGDQQAQWFGAGTGGYLSPEVLRKDPYK 180
QY      194 PYDIWACGVILYLLVGYPPFWDQKHLYQOIKAGAYDPPSPWDVTPPAKLNINQML 253
Db      181 PYDIWACGVILYLLVGYPPFWDQKHLYQOIKAGAYDPPSPWDVTPPAKLNINQML 240
QY      254 TINPAKRITAEALKHPWQCORSTVASMHRQETVECLKFNARKLKGA1ITM 308
Db      241 TINPAKRITADQALKHPWQCORSTVASMHRQETVECLKFNARKLKGA1ITM 295

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
                    INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,422
FILING DATE: 11-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241

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/
/ REFERENCE/DOCKET NUMBER: S-18805H
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (919)541-8587
/ TELEFAX: (919)541-8689
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 295 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ FEATURE:
/ NAME/KEY: Protein
/ LOCATION: 1..295
/ OTHER INFORMATION: /note= "rat protein kinase II
/ protein sequence as shown in Figure 32."
/ SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-547-422-23

Query Match 53.4%; Score 1450; DB 4; Length 295;
Best Local Similarity 92.5%; Pred. No. 9.6e-131;
Matches 273; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 14 YQLYEDIGKGFVSRVRCVKLTGHEVAAKIINTKLSARDHOKLREARICRLKHSNI 73
DB 1 YQLYEDIGKGFVSRVRCVKLTGHEVAAKIINTKLSARDHOKLREARICRLKHPNI 60
QY 74 VLHDSISEGFFHYLVFDTVTGGELFEDIIVAREYYSADASHCIQQLLEAVLCHOMGVV 133
DB 61 VLHDSISEGFFHYLVFDTVTGGELFEDIIVAREYYSADASHCIHQLESVNIHQDIV 120
QY 134 HRDLKPENLLASCKGKRAVKLADFGLAIEVQDQQAQWFGAGTGGYLSPEVLKQAYGK 193
DB 121 HRDLKPENLLASCKGKRAVKLADFGLAIEVQGEQAQWFGAGTGGYLSPEVLKQPYGK 180
QY 194 PVDIWAGVILYILVGYPPFPWDEDOHKLQKQIKAGAYDPPSPEDWDTVTPKNNLNQ 253
DB 181 PVDIWAGVILYILVGYPPFPWDEDOHKLQKQIKAGAYDPPSPEDWDTVTPKNNLNQ 240
QY 254 TTNPAKRITAEALKHPWVQCORSTVASMHRQETVECLKFNARKLKGAILTTM 308
DB 241 TTNPAKRITAEALKHPWVQCORSTVASMHRQETVECLKFNARKLKGAILTTM 295

RESULT 9
US-07-857-224B-19
/ Sequence 19, Application US/07857224B
/ Patent No. 5958784
/ GENERAL INFORMATION:
/ APPLICANT: Benner, Steven A.
/ TITLE OF INVENTION: Predicting Folded Structures of Proteins
/ NUMBER OF SEQUENCES: 114
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Steven A. Benner
/ STREET: Hadlaubstrasse 151
/ CITY: Zurich
/ STATE: none
/ COUNTRY: Switzerland
/ ZIP: (note: this is an international post code) CH-8092
/ MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
/ COMPUTER: Apple Macintosh
/ OPERATING SYSTEM: Macintosh 7.0
/ SOFTWARE: Microsoft Word
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/857,224B
/ FILING DATE: 03/25/92
/ CLASSIFICATION: 436
/ PRIOR APPLICATION DATA: none
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (International) 41 1 632 2830
/ TELEFAX: (International) 41 1 262 2437
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/
/ TELEX: none
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 264
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ DESCRIPTION: protein
/ ORIGINAL SOURCE:
/ ORGANISM: rat
/ FEATURE: Protein kinase; Table 8 Column 21
/ PUBLICATION INFORMATION:
/ AUTHORS:
/ AUTHORS: Hanks, S. K.
/ AUTHORS: Quinna, A. M.
/ AUTHORS: Hunter, T.
/ TITLE: The protein kinase family
/ JOURNAL: Science
/ VOLUME: 241
/ PAGES: 42-52
/ DATE: 1988
/ US-07-857-224B-19

Query Match 51.7%; Score 1405; DB 2; Length 264;
Best Local Similarity 99.6%; Pred. No. 1.7e-126;
Matches 263; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 DEQLYEDIGKGFVSRVRCVKLTGHEVAAKIINTKLSARDHOKLREARICLLKHS 71
DB 1 DEQLYEDIGKGFVSRVRCVKLTGHEVAAKIINTKLSARDHOKLREARICLLKHS 60
QY 72 NIVRLHDSISEGFFHYLVFDTVTGGELFEDIIVAREYYSADASHCIQQLLEAVLCHOMG 131
DB 61 NIVRLHDSISEGFFHYLVFDTVTGGELFEDIIVAREYYSADASHCIQQLLEAVLCHOMG 120
QY 132 VVERDLKPENLLASCKGKRAVKLADFGLAIEVQDQQAQWFGAGTGGYLSPEVLKQAY 191
DB 121 VVERDLKPENLLASCKGKRAVKLADFGLAIEVQDQQAQWFGAGTGGYLSPEVLKQAY 180
QY 192 GKPDVWAGVILYILVGYPPFPWDEDOHKLQKQIKAGAYDPPSPEDWDTVTPKNNLNQ 251
DB 181 GKPDVWAGVILYILVGYPPFPWDEDOHKLQKQIKAGAYDPPSPEDWDTVTPKNNLNQ 240
QY 252 MLTINPAKRITAEALKHPWVQCOR 275
DB 241 MLTINPAKRITAEALKHPWVQCOR 264

RESULT 10
US-07-857-224B-18
/ Sequence 18, Application US/07857224B
/ Patent No. 5958784
/ GENERAL INFORMATION:
/ APPLICANT: Benner, Steven A.
/ TITLE OF INVENTION: Predicting Folded Structures of Proteins
/ NUMBER OF SEQUENCES: 114
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Steven A. Benner
/ STREET: Hadlaubstrasse 151
/ CITY: Zurich
/ STATE: none
/ COUNTRY: Switzerland
/ ZIP: (note: this is an international post code) CH-8092
/ MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
/ COMPUTER: Apple Macintosh
/ OPERATING SYSTEM: Macintosh 7.0
/ SOFTWARE: Microsoft Word
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/857,224B
/ FILING DATE: 03/25/92
/ CLASSIFICATION: 436
/ PRIOR APPLICATION DATA: none
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;
; LENGTH: 370 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 790790
; US-08-878-989-19

Query Match          21.5%; Score 583; DB 2; Length 370;
Best Local Similarity 39.1%; Pred. No. 1.9e-47;
Matches 133; Conservative 57; Mismatches 126; Indels 24; Gaps 8;

QY 12 DEYQLYEDIGKGFASV-----RCVKLCGTCGHEVYAAKIINTKLSARDHOKLERARICR 66
Db 18 DIYDFRDLVGTGAFSEVILAEKRTQKL-----VAIKCIAKEALEGKE-GSMENEIAVLH 71

QY 67 LKHSNIVRLHDSISEGFH-YLVFDLVGGELFEDIVAREYVSEADASHCICQILEAVL 125
Db 72 KIKHPNIVAL-DDIYESGGHLYLIMQVSGGELFDRIVEKGFYTERDASRLIFQVLDAYK 130

QY 126 HCHQMGVVRHDLKPENLLIASKCGAAVKLADFLGLAIEVQDQQAQWFGAGTGGYLSPEV 185
Db 131 YLHDLGIVHRDLKPENLLYSLDESDSKIMISDFGLS-KMEDPGSVLSTACGTGGYVAPEV 189

QY 186 LRKEAYGKPDVWACGVILYLLGVYPPFWDQDQKLYQIKAGAYDFPSPENDTVPPEA 245
Db 190 LAQPYSKAVDCWSIGVIAYILLCGYPFFYDENDAKLFQILKAEYEDFSYWDIDSDA 249

QY 246 KNLINQMLTINPAKRITAHEALKHPWCQSTVASMHRQETVECLKFNARRKLKGAIL 305
Db 250 KDFIRHLMKDPKRFCTCEQALQHPWIAGTALDKNIH-QSVSEQIKKNFAKSKWQAQFN 308

QY 306 TT-----MLATRNFSVGRQTTPATMTSTAASGTTMG 336
Db 309 ATAVVRHMRKLQIGTSQEGQGTASGHGELLTPVAGGPAAG 348
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RESULT 13
US-09-272-796-19
; Sequence 19, Application US/09272796
; Patent No. 6207148
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,796
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/878,989
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
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;
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 370 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 790790
; US-09-272-796-19

Query Match          21.5%; Score 583; DB 3; Length 370;
Best Local Similarity 39.1%; Pred. No. 1.9e-47;
Matches 133; Conservative 57; Mismatches 126; Indels 24; Gaps 8;

QY 12 DEYQLYEDIGKGFASV-----RCVKLCGTCGHEVYAAKIINTKLSARDHOKLERARICR 66
Db 18 DIYDFRDLVGTGAFSEVILAEKRTQKL-----VAIKCIAKEALEGKE-GSMENEIAVLH 71

QY 67 LKHSNIVRLHDSISEGFH-YLVFDLVGGELFEDIVAREYVSEADASHCICQILEAVL 125
Db 72 KIKHPNIVAL-DDIYESGGHLYLIMQVSGGELFDRIVEKGFYTERDASRLIFQVLDAYK 130

QY 126 HCHQMGVVRHDLKPENLLIASKCGAAVKLADFLGLAIEVQDQQAQWFGAGTGGYLSPEV 185
Db 131 YLHDLGIVHRDLKPENLLYSLDESDSKIMISDFGLS-KMEDPGSVLSTACGTGGYVAPEV 189

QY 186 LRKEAYGKPDVWACGVILYLLGVYPPFWDQDQKLYQIKAGAYDFPSPENDTVPPEA 245
Db 190 LAQPYSKAVDCWSIGVIAYILLCGYPFFYDENDAKLFQILKAEYEDFSYWDIDSDA 249

QY 246 KNLINQMLTINPAKRITAHEALKHPWCQSTVASMHRQETVECLKFNARRKLKGAIL 305
Db 250 KDFIRHLMKDPKRFCTCEQALQHPWIAGTALDKNIH-QSVSEQIKKNFAKSKWQAQFN 308

QY 306 TT-----MLATRNFSVGRQTTPATMTSTAASGTTMG 336
Db 309 ATAVVRHMRKLQIGTSQEGQGTASGHGELLTPVAGGPAAG 348

RESULT 14
US-09-457-040B-31
; Sequence 31, Application US/09457040B
; Patent No. 6387641
; GENERAL INFORMATION:
; APPLICANT: Vertex Pharmaceuticals Incorporated
; APPLICANT: Bellon, Steve
; TITLE OF INVENTION: Crystallized P38 Complexes
; FILE REFERENCE: WPI/98-14
; CURRENT APPLICATION NUMBER: US/09/457,040B
; CURRENT FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Human
; US-09-457-040B-31

Query Match          21.5%; Score 583; DB 4; Length 370;
Best Local Similarity 39.1%; Pred. No. 1.9e-47;
Matches 133; Conservative 57; Mismatches 126; Indels 24; Gaps 8;

QY 12 DEYQLYEDIGKGFASV-----RCVKLCGTCGHEVYAAKIINTKLSARDHOKLERARICR 66
Db 18 DIYDFRDLVGTGAFSEVILAEKRTQKL-----VAIKCIAKEALEGKE-GSMENEIAVLH 71
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D6 730 PGEAVPAPTPESTPHCP 748

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Db	72	KIHPNIVAL-DDIYESGGHYLIINQYVSGGELFDRIVEKGFYTERDASRLIFQVLDVAK	130
QY	126	HCQMGGVHRDLKENILLASKCKGAANKLADGLAEIWEQGDQANWFGPACTPGVLSPEV	185
Db	131	YLHDLGIHVHRLKENLILYSDDESKIMISDFRGLS-KMEDPGSVLSTACGTPGVYAFV	189
QY	186	LREAKGPVDINACGVILYLLNGYPPFWDEQHKLYQTKAGANDPSPEDWTVPPEA	245
Db	190	LAQPKYSKAVDCWISGVIAIYLLICGYPPFYDENDAKLFEELIKAEYFESPWDDISDA	249
QY	246	KNLINQMILTINPAKRITTAHEALKHPWQCQSTVASMHRQETVECLIKKNARKKLKGAIL	305
Db	250	KDFIRLHEKDPERRFTCEQALQHPWIAGTALDKNIH-QSVSEQIKKKFAKSKWKQAFN	308
QY	306	TT-----MLATRNFSVGROTTAPATMSTAASCTMG	336
Db	309	ATAVVRHMKLLOLCTSOEGOGOTASHGELLTPVAGPAAAG	348

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RESULT 15
US-09-975-326-4
; Sequence 4, Application US/09975326
; Patent No. 6476210
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; TITLE OF INVENTION: No. 6476210el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0254-USA
; CURRENT APPLICATION NUMBER: US/09/975,326
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/239,821
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 765
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-975-326-4

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Query Match	21.4%;	Score 582;	DB 4;	Length 765;
Best Local Similarity	34.6%;	Pred. No. 7.4e-47;		
Matches 131;	Conservative 70;	Mismatches 154;	Indels 24;	Gaps 6;
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DB	391	EKKYIGKVGDFGNFAVKECIDRSTGKEFPALKIIDKAKCCGKEH-LIENEVSLIRVKIP	449	
QY	72	NIVRLHDSISEEGFHVDFDLVTGELFEDIVAREYISEADASHCIQOILELVHCHQM	131	
DB	450	NIIMLVEEMETAFELFVMEVLWKGDFLDAITSSTKYTERDGSAMYNLANALRYLHG	509	
QY	132	VVHRLDPENLLIASCKGA-AVKLAFGLAIEVQGDQAMFGFAGPGLSPEVURKEA	190	
DB	510	IIVHRDKPENLLICEYPDGTSKLKGLDFGLATVEG---PLTYVCGPTTVAPEIIAETG	566	
QY	191	YCKPVDIWAAGVILYTLINGYPPFWDED--QHKLYQIIOIKAGAYDFPSPWDVTPPAKML	248	
DB	567	YGLKVDIWAAGVITYILLCGFPFPRSENNIQEDLFQIILAGLKEFPAPYDNTDTSAKEL	626	
QY	249	INQMLTINPAKRITAEHALKHPWVCRSTVASMHHQVEVECLKFNARRKLGAILTMM	308	
DB	627	ISQMLQVNVYARCTAGLISHFWSDSDASNNMQAEVITGKLQHNFNALPKONSTTGV	686	
QY	309	LATRNFVSGHQTAPATMSTAASGTTMGLVEQAKSLINKKADGVKPTNSTKNASAAATP	368	
DB	687	SYMIMTALDKE-----GQIFCSKHQODSGREGMEP-ISPVPFSVEIYP	729	
QY	369	KGTLPAPALPEQTTVIHNP	387	

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(without alignments)  
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Title: US-09-820-790B-2  
Perfect score: 2715  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
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Total number of hits satisfying chosen parameters: 600653  
Minimum DB seq length: 0  
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Maximum Match 100%  
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14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
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18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	2205	81.2	556	14	US-10-096-960-4
5	2070	76.2	499	12	US-10-354-358-88
6	1450	53.4	295	11	US-09-988-462-23
7	1174	43.2	261	9	US-09-925-299-983
8	1174	43.2	261	11	US-09-925-299-983
9	619.5	22.8	355	12	US-10-325-975-10
10	616	22.7	473	12	US-10-320-351-15
11	613.5	22.6	357	15	US-10-024-036B-2
12	584.5	21.5	460	11	US-09-935-464-3
13	584.5	21.5	460	15	US-10-125-835-3
14	584.5	21.5	476	11	US-09-935-464-5
15	584.5	21.5	476	15	US-10-125-835-5

16	583	21.5	370	10	US-09-817-181-4	Sequence 4, Appli
17	583	21.5	370	12	US-09-769-970-19	Sequence 19, Appli
18	583	21.5	370	12	US-10-090-002-4	Sequence 4, Appli
19	583	21.5	370	12	US-10-204-041-10	Sequence 10, Appli
20	583	21.5	370	15	US-10-142-356-7	Sequence 7, Appli
21	583	21.5	370	15	US-10-300-828-4	Sequence 4, Appli
22	582	21.4	765	10	US-09-975-326-4	Sequence 4, Appli
23	582	21.4	765	15	US-10-217-357-4	Sequence 4, Appli
24	582	21.4	766	10	US-09-975-326-2	Sequence 2, Appli
25	582	21.4	766	10	US-09-934-406-2	Sequence 2, Appli
26	582	21.4	766	12	US-10-170-789-21	Sequence 21, Appli
27	582	21.4	766	15	US-10-217-357-2	Sequence 2, Appli
28	577.5	21.3	317	11	US-09-935-464-36	Sequence 36, Appli
29	577.5	21.3	317	15	US-10-125-835-36	Sequence 36, Appli
30	566.5	20.9	495	12	US-10-289-172-1	Sequence 1, Appli
31	566.5	20.9	495	12	US-09-848-806-1	Sequence 1, Appli
32	561.5	20.7	501	12	US-10-289-172-3	Sequence 3, Appli
33	561.5	20.7	501	12	US-09-848-806-3	Sequence 3, Appli
34	558	20.6	463	11	US-09-988-462-25	Sequence 25, Appli
35	519	20.2	406	10	US-09-771-161A-210	Sequence 210, Appli
36	549	20.2	639	10	US-09-854-731-17	Sequence 17, Appli
37	546.5	20.1	326	10	US-09-817-181-2	Sequence 2, Appli
38	546.5	20.1	326	12	US-10-090-002-2	Sequence 2, Appli
39	546.5	20.1	326	15	US-10-300-828-2	Sequence 2, Appli
40	546	20.1	501	14	US-10-153-921-2	Sequence 2, Appli
41	545	20.1	501	9	US-09-797-039-2	Sequence 2, Appli
42	545	20.1	501	12	US-10-170-789-2	Sequence 2, Appli
43	542.5	20.0	343	12	US-09-769-970-5	Sequence 5, Appli
44	541	19.9	254	11	US-09-898-837A-38	Sequence 38, Appli
45	541	19.9	648	15	US-10-024-036B-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1  
US-09-820-790-2  
; Sequence 2, Application US/09820790  
; Publication No. US20030140354A1  
; GENERAL INFORMATION:  
; APPLICANT: SHAO, Wei et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CLO01204  
; CURRENT APPLICATION NUMBER: US/09/820,790  
; CURRENT FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 516  
; TYPE: PPT  
; ORGANISM: Human  
US-09-820-790-2

Query Match	100.0%;	Score 2715;	DB 12;	Length 516;
Best Local Similarity	100.0%;	Pred. No. 1.3e-217;		
Matches 516;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MATTVTCTRTDYEYQIYEDI	IGKGFVSVVRVCVKICTGHEYYAAKIINTKLSARDHQKLER	60
Db	1	MATTVTCTRTDYEYQIYEDI	IGKGFVSVVRVCVKICTGHEYYAAKIINTKLSARDHQKLER	60
Qy	61	EARICRLKHSNIVRLHDSIS	EEGPHYLVDTVTGGELFEDIVAREYYSEADASHCICQI	120
Db	61	EARICRLKHSNIVRLHDSIS	EEGPHYLVDTVTGGELFEDIVAREYYSEADASHCICQI	120
Qy	121	LEAVLHCHQGVVHRDLKPFEN	LLASKCKGAAYKADFGLAIEVQDQOQAFAGPGY	180
Db	121	LEAVLHCHQGVVHRDLKPFEN	LLASKCKGAAYKADFGLAIEVQDQOQAFAGPGY	180
Qy	181	LSPEVLRKRAYGKVPDINAC	GVILLYLLVGYPPFWDEDQHKLYQIKAGAYDFSPEND	240
Db	181	LSPEVLRKRAYGKVPDINAC	GVILLYLLVGYPPFWDEDQHKLYQIKAGAYDFSPEND	240

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Db 181 LSPVLRKEAYGKPVDIWACGVILYLLVGPFPFWEDEQHKLYQOIKAGAYDPPSPWD 240
QY 241 VTPEAKNLINOMLTINPAKRITAEALKHPWCQSTVASMMHROETVECLKKNARRKL 300
Db 241 VTPEAKNLINOMLTINPAKRITAEALKHPWCQSTVASMMHROETVECLKKNARRKL 300
QY 301 KGAILTMTATRNFSVGRQTTAPATMTASTAGTTMGLVQAKSLNKKADGVKQPNSTK 360
Db 301 KGAILTMTATRNFSVGRQTTAPATMTASTAGTTMGLVQAKSLNKKADGVKQPNSTK 360
QY 361 NSAAATSPKGTLPAALEPQTTVHNPNVDGKESDSANTTIEDAKARKOEIKTTEQ 420
Db 361 NSAAATSPKGTLPAALEPQTTVHNPNVDGKESDSANTTIEDAKARKOEIKTTEQ 420
QY 421 LIEAVNNGDFEAYAFYFENLLAKNSKPIHTTILNPHVHVGEDACIAYIRLQYIDGOG 480
Db 421 LIEAVNNGDFEAYAFYFENLLAKNSKPIHTTILNPHVHVGEDACIAYIRLQYIDGOG 480
QY 481 RPRTSQSEETRVWHRDQKQWVHFHCGSGAPVAPLQ 516
Db 481 RPRTSQSEETRVWHRDQKQWVHFHCGSGAPVAPLQ 516

RESULT 2
US-09-820-790-4
; Sequence 4, Application US/09820790
; Publication No. US20030140354A1
; GENERAL INFORMATION:
; APPLICANT: SHAO, Wei et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001204
; CURRENT APPLICATION NUMBER: US/09/820,790
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Human
US-09-820-790-4

Query Match 99.2%; Score 2692; DB 12; Length 542;
Best Local Similarity 95.2%; Pred. No. 1.1e-315;
Matches 516; Conservative 0; Mismatches 0; Indels 26; Gaps 1;

QY 1 MATVTCTRTFDEQLYEDIGKGFVSVRCVKLCTGHEYAAKIINTKKLSARDHOKLER 60
Db 1 MATVTCTRTFDEQLYEDIGKGFVSVRCVKLCTGHEYAAKIINTKKLSARDHOKLER 60
QY 61 EARICRLKHSNIVRLHDSISEGPHYLVDLVGTGELFEDIVAREYIYSEADASHCICQI 120
Db 61 EARICRLKHSNIVRLHDSISEGPHYLVDLVGTGELFEDIVAREYIYSEADASHCICQI 120
QY 121 LEAVLHCHQGVVHRLKPNELLASKCKGAAYKADFGLAIEVQDQQAQAFGAGTGGY 180
Db 121 LEAVLHCHQGVVHRLKPNELLASKCKGAAYKADFGLAIEVQDQQAQAFGAGTGGY 180
QY 181 LSPVLRKEAYGKPVDIWACGVILYLLVGPFPFWEDEQHKLYQOIKAGAYDPPSPWD 240
Db 181 LSPVLRKEAYGKPVDIWACGVILYLLVGPFPFWEDEQHKLYQOIKAGAYDPPSPWD 240
QY 241 VTPEAKNLINOMLTINPAKRITAEALKHPWCQSTVASMMHROETVECLKKNARRKL 300
Db 241 VTPEAKNLINOMLTINPAKRITAEALKHPWCQSTVASMMHROETVECLKKNARRKL 300
QY 301 KGAILTMTATRNFSVGRQTTAPATMTASTAGTTMGLVQAKSLNKKADGVKQPNSTK 360
Db 301 KGAILTMTATRNFSVGRQTTAPATMTASTAGTTMGLVQAKSLNKKADGVKQPNSTK 360
QY 361 NSAAATSPKGTLPAALEPQTTVHNPNVDGKESDSANTTIEDAKARKOEIKTTEQ 420

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Db 361 NSAAATSPKGTLPAALEPQTTVHNPNVDGKESDSANTTIEDAKARKOEIKTTEQ 420
QY 421 LIEAVNNGDFEAYAFYFENLLAKNSKPIHTTILNPHVHVGEDACIAYIRLQYIDGOG 480
Db 421 LIEAVNNGDFEAYAFYFENLLAKNSKPIHTTILNPHVHVGEDACIAYIRLQYIDGOG 480
QY 481 RPRTSQSEETRVWHRDQKQWVHFHCGSGAPVAPLQ 516
Db 481 RPRTSQSEETRVWHRDQKQWVHFHCGSGAPVAPLQ 516

RESULT 3
US-10-096-960-2
; Sequence 2, Application US/10096960
; Publication No. US20020132325A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001158D1V
; CURRENT APPLICATION NUMBER: US/10/096,960
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 09/800,960
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 565
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-096-960-2

Query Match 82.0%; Score 2225.5; DB 14; Length 565;
Best Local Similarity 74.7%; Pred. No. 8.6e-177;
Matches 434; Conservative 30; Mismatches 36; Indels 81; Gaps 5;

QY 1 MATVTCTRTFDEQLYEDIGKGFVSVRCVKLCTGHEYAAKIINTKKLSARDHOKLER 60
Db 1 MATVTCTRTFDEQLYEDIGKGFVSVRCVKLCTGHEYAAKIINTKKLSARDHOKLER 60
QY 61 EARICRLKHSNIVRLHDSISEGPHYLVDLVGTGELFEDIVAREYIYSEADASHCICQI 120
Db 61 EARICRLKHSNIVRLHDSISEGPHYLVDLVGTGELFEDIVAREYIYSEADASHCICQI 120
QY 121 LEAVLHCHQGVVHRLKPNELLASKCKGAAYKADFGLAIEVQDQQAQAFGAGTGGY 180
Db 121 LEAVLHCHQGVVHRLKPNELLASKCKGAAYKADFGLAIEVQDQQAQAFGAGTGGY 180
QY 181 LSPVLRKEAYGKPVDIWACGVILYLLVGPFPFWEDEQHKLYQOIKAGAYDPPSPWD 240
Db 181 LSPVLRKEAYGKPVDIWACGVILYLLVGPFPFWEDEQHKLYQOIKAGAYDPPSPWD 240
QY 241 VTPEAKNLINOMLTINPAKRITAEALKHPWCQSTVASMMHROETVECLKKNARRKL 300
Db 241 VTPEAKNLINOMLTINPAKRITAEALKHPWCQSTVASMMHROETVECLKKNARRKL 300
QY 301 KGAILTMTATRNFSVGRQTTAPATMTASTAGTTMGLVQAKSLNKKADGVKQPNSTK 359
Db 301 KGAILTMTATRNFSVGRQTTAPATMTASTAGTTMGLVQAKSLNKKADGVKQPNSTK 359
QY 360 KNSAAATSPKGTLPAALEPQTTVHNPNVDGKESDSANTTIEDAKARKOEIKTTEQ 409
Db 360 KNSAAATSPKGTLPAALEPQTTVHNPNVDGKESDSANTTIEDAKARKOEIKTTEQ 409
QY 410 -----VKQETIITKTEQLIEAVNNGDFEAYAFYFENLLAKNSKPIHTTILNPHVHVGEDACIAYIRLQYIDGOG 434
Db 410 -----VKQETIITKTEQLIEAVNNGDFEAYAFYFENLLAKNSKPIHTTILNPHVHVGEDACIAYIRLQYIDGOG 434
QY 405 VPEGRSRRDTAPSAGMOPQPSLCSSAMRKQBIITKTEQLIEAVNNGDFEAYAFYFENLLAKNSKPIHTTILNPHVHVGEDACIAYIRLQYIDGOG 464
Db 405 VPEGRSRRDTAPSAGMOPQPSLCSSAMRKQBIITKTEQLIEAVNNGDFEAYAFYFENLLAKNSKPIHTTILNPHVHVGEDACIAYIRLQYIDGOG 464

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Db      516 IDQGGRPTSOSETRVWHRRDGLWLNWHVHCSAPAPLQ 556
RESULT 5
US-10-354-358-88
/ Sequence 88, Application US/10354358
/ Publication No. US20030157082A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc
/ APPLICANT: Hunter, John Joseph
/ APPLICANT: MacBeth, Kyle J.
/ APPLICANT: Tsai, Fong-Ying
/ APPLICANT: Lesoon, Andrea
/ APPLICANT: Lightcap, Eric S.
/ APPLICANT: Williamson, Mark
/ APPLICANT: Rudolph-Owen, Laura A.
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
/ TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089,
/ TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 88
/ TITLE OF INVENTION: 3703, 14171, 10359, 1650, 1450, 188
/ TITLE OF INVENTION: 9252, 9389, 1642, 83269, 10297, 158
/ TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 208
/ TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21
/ TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 2744
/ FILE REFERENCE: MP102-020P18NOMNTM
/ CURRENT APPLICATION NUMBER: US/10/354,358
/ CURRENT FILING DATE: 2003-01-30
/ PRIOR APPLICATION NUMBER: US 60/353,600
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 60/364,517

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> PRIOR FILING DATE: 2002-03-19
> PRIOR APPLICATION NUMBER: US 60/371,075
> PRIOR FILING DATE: 2002-04-09
> PRIOR APPLICATION NUMBER: US 60/371,507
> PRIOR FILING DATE: 2002-04-10
> PRIOR APPLICATION NUMBER: US 60/372,984
> PRIOR FILING DATE: 2002-04-16
> PRIOR APPLICATION NUMBER: US 60/374,194
> PRIOR FILING DATE: 2002-04-19
> PRIOR APPLICATION NUMBER: US 60/382,995
> PRIOR FILING DATE: 2002-05-24
> PRIOR APPLICATION NUMBER: US 60/385,023
> PRIOR FILING DATE: 2002-05-31
> PRIOR APPLICATION NUMBER: US 60/386,853
> PRIOR FILING DATE: 2002-06-14
> PRIOR APPLICATION NUMBER: US 60/389,395
> PRIOR FILING DATE: 2002-06-17
> Remaining Prior Application data removed - See File Wrapper or PALM.
> NUMBER OF SEQ ID NOS: 122
> SOFTWARE: FastSeq for Windows Version 4.0
> SEQ ID NO 88
> LENGTH: 499
> TYPE: PRT
> ORGANISM: Homo sapiens
US-10-354-358-88

Query Match          76.2%; Score 2070; DB 12; Length 499;
Best Local Similarity 73.1%; Pred. No. 6.4e-164;
Matches 396; Conservative 31; Mismatches 25; Indels 90; Gaps 3;

Qy      1  MATTVTCTRTDEYQLVEDIGKGAFSVVRCKVLCITGHEYAAKINTKKLSARDHOKLER 60
Db      1  MASTTCTRTDEYQLFELGKGAFSVVRCKMKTGGGYAAKINTKKLSARDHOKLER 60

Qy      61  EATCRLLKHSNIVRLHDSISEEGFHYLVPDLVTGSELFEDIVAREYYSADASHCIQOI 120
Db      61  EATCRLLKHPNIVRLHDSISEEGFHYLVPDLVTGSELFEDIVAREYYSADASHCIQOI 120

Qy      121  LEAVLHCHGVVHRDLKPENLLILASKCKGAAYKVLADFLGIAIEVGQDQAWFGFAGTPGY 180
Db      121  LESVNVHCHGVVHRDLKPENLLILASKGAAVKVLADFLGIAIEVGQDQAWFGFAGTPGY 180

Qy      181  LSPVLRKEAYGKPDFINWACGVILYLLVGYPPFDEQDQHKLYOOIKAGAYOFFPSPEDWT 240

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; NAME/KEY: SITE
; LOCATION: (259)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (260)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-983

Query Match      43.2%; Score 1174; DB 9; Length 261;
Best Local Similarity 73.5%; Pred. No. 1.le-89;
Matches 230; Conservative 11; Mismatches 8; Indels 64; Gaps 2;

QY 93 VTGGELFEDIVAREYSEADASHCIQQLLEAVLHCHOMGVVHRDLKPENLLASKCKGAA 152
Db 1 VTGGELFEDIVAREYSEADASHCIQQLLEAVLHCHOMGVVHRDLKPENLLASKCKGAA 60
QY 153 VKLADFGLAIEVQDQQAWEFGAGTGGYLSPEVLRKEAYGKPDVDIWAQGVILYLLVGYP 212
Db 61 VKLADFGLAIEVQDQQAWEFGAGTGGYLSXXVLKDPYKPDVMMWAGVILYLLVGYP 120
QY 213 PFWDEDQHLKIQKAGAYDFPSPEDWTVTPEAKNLINOMLTINPAKRITAEALKHPWV 272
Db 121 PFWDEDQHLKIQKAGAYDFPSPEDWTVTPEAKNLINOMLTINPAKRITAEALKHPWI 180
QY 273 CORSTVASMHRQETVECLKFNARKLKGAILLTMTLATRNFSVGRQTTAPATMSTAASG 332
Db 181 CORSTVASMHRQETVECLKFNARKLKGAILLTMTLATRNFSVGRQTTAPATMSTAASG 224
QY 333 TTMGLVQAKSLLNKKADGVKPTQNTSKNSAAATSPKGTLPAALEPQTTVIHNPVDGK 392
Db 225 -----AKSLKKP-----
QY 393 ESSDSANTTIEDE 405
Db 237 ESTESSNTTIEDE 249

RESULT 8
US-09-925-299-983
; Sequence 983, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 983
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (91)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (92)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (259)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (260)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-983

Query Match      43.2%; Score 1174; DB 11; Length 261;
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Best Local Similarity 73.5%; Pred. No. 1.le-89;
Matches 230; Conservative 11; Mismatches 8; Indels 64; Gaps 2;

QY 93 VTGGELFEDIVAREYSEADASHCIQQLLEAVLHCHOMGVVHRDLKPENLLASKCKGAA 152
Db 1 VTGGELFEDIVAREYSEADASHCIQQLLEAVLHCHOMGVVHRDLKPENLLASKCKGAA 60
QY 153 VKLADFGLAIEVQDQQAWEFGAGTGGYLSPEVLRKEAYGKPDVDIWAQGVILYLLVGYP 212
Db 61 VKLADFGLAIEVQDQQAWEFGAGTGGYLSXXVLKDPYKPDVMMWAGVILYLLVGYP 120
QY 213 PFWDEDQHLKIQKAGAYDFPSPEDWTVTPEAKNLINOMLTINPAKRITAEALKHPWV 272
Db 121 PFWDEDQHLKIQKAGAYDFPSPEDWTVTPEAKNLINOMLTINPAKRITAEALKHPWI 180
QY 273 CORSTVASMHRQETVECLKFNARKLKGAILLTMTLATRNFSVGRQTTAPATMSTAASG 332
Db 181 CORSTVASMHRQETVECLKFNARKLKGAILLTMTLATRNFSVGRQTTAPATMSTAASG 224
QY 333 TTMGLVQAKSLLNKKADGVKPTQNTSKNSAAATSPKGTLPAALEPQTTVIHNPVDGK 392
Db 225 -----AKSLKKP-----
QY 393 ESSDSANTTIEDE 405
Db 237 ESTESSNTTIEDE 249

RESULT 9
US-10-355-975-10
; Sequence 10, Application US/10355975
; Publication No. US20030162277A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
; FILE REFERENCE: 2923-A
; CURRENT APPLICATION NUMBER: US/10/355,975
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US/09/579,664B
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 10
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-355-975-10

Query Match      22.8%; Score 619.5; DB 12; Length 355;
Best Local Similarity 39.5%; Pred. No. 2.6e-43;
Matches 131; Conservative 62; Mismatches 124; Indels 15; Gaps 5;

QY 14 YQLYEDIGKGAFTSVRRVYKLTCTGHEGYAAKLTINTKLSARDHQKLERBARICLLKHSNI 73
Db 23 PFEKETLTGAGFSEVVLAEKATGKLFVAKCIPKALKGKE--STENEAIVLRKIKHENI 81
QY 74 VRLHDSISEGPHLYFDVLTGGELEFEDIVAREYSEADASHCIQQLLEAVLHCHOMGVV 133
Db 82 VALEDIVESPNHLYLMQVLSGGELFDRIEKGFTYKDASTLIRQVLDAYVYLHRMGIV 141
QY 134 HRDLKPENLLASKCKGAAVKLADFGALAEVQDQQAWEFGAGTGGYLSPEVLRKEAYGK 193
Db 142 HRDLKPENLLYQSDRESKIMISDFGLS--XMEKGDVNSTAGTCFGYVAPVLAQKPYK 200
QY 194 PVDIWAQGVILYLLGYFPFWDEDQHLKIQKAGAYDFPSPEDWTVTPEAKNLINOML 253
Db 201 AVDCWSIGVIAYILLOGYPPFYDENDSKLFQILKAEYEFDSFYWDIDISAKDFINLM 260
QY 254 TINPAKRITAEALKHPWVCORSTVASMHRQETVECLK-----FNAR----RKLK 301
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; APPLICANT: Meyer, Joanne
; APPLICANT: Barrington-Martin, Rory
; APPLICANT: Parker, Alexander
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING
; TITLE OF INVENTION: NEUROPSYCHIATRIC
; TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
; FILE REFERENCE: 3322/0H702 USO
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US/09/757,300
; PRIOR FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-835-5

Query Match      21.5%; Score 584.5; DB 15; Length 476;
Best Local Similarity 35.8%; Pred. No. 3.2e-40;
Matches 137; Conservative 63; Mismatches 142; Indels 41; Gaps 8;

QY      8  TRETDEYQLVEDIGKAFSVRRCKVLCCTGHEVAAKIINTKKLSARDHOKLREARICRL 67
DB      17  TNIRKTFIFNEVLGSGAFSEVPLVKQRLTGKLFALKCI--KKSPAFRDSSELEIAVLKK 74

QY      68  LKHSNIVLHDSISEGPHYLVDLVGTGGELFEDIVAREYSEADASHCIQOILEAVLHC 127
DB      75  IKHENIVTLEDIYESTTHYLVMLVSGGELFDRILRGVYTEKDASLVIQOVL SAVKYL 134

QY      128  HONGVYVHRDLKPENLILASKCAAVKLADFLGA-IEVQGDQOAWFGAGTGGYLSPEVL 186
DB      135  HENGIVNRDLKPENLILYLPENSIMITDEGLSKMEQNGIMST---ACGTPGYVAPEVL 191

QY      187  RKEAYGKVPDIWACGVILYILVGYPPFWEDEQHKLYQIKAGAYDFPSPEDWTVWPEAK 246
DB      192  AOKPYSKAVDCWSIGVITVILCGYPPFYEETESKLFKEIKGYEFEPFSPFWDIDISESAK 251

QY      247  NLINOMLAINPAKRTAHALKHPWVCORSTVASMHRQETVCECLKKNARRKLKGAILT 306
DB      252  DFICHLLEKDPNEYTCERKALSHPWIDGNALHRDIYPSVSIQIKNP-AKSKWRQAF-- 308

QY      307  TMLATRNFSVGRQTTAPATMSTAASGTTMGLVEQAKSL-LNKKADGVKPKQTNSTKNSAAA 365
DB      309  -----NAAAVVHHMRKLMHNLHSPGVRPE---VENRPPPE 339

QY      366  TSPKGLPPLPAALEPQTVIHNVPV 388
DB      340  TQASTSRSFSS--PEITITEAPV 360

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